

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:20:05 ; Search time 36 Seconds
(without alignments)
799.504 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCGVHVTKEVKEVA.....LRVNOTFNWTTQEHPPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

ID	Score	Match	Length	DB	ID	Description
1	1149	100.0	288	16	AAR67989	Human B lymphocyte
2	1149	100.0	288	18	AAW38414	B7-1. Homo sapien
3	1149	100.0	288	20	AAW67804	Human B7 protein s
4	1149	100.0	288	20	AAW73640	Human B7-2 antigen
5	1149	100.0	288	21	AAW37087	Human B lymphocyte
6	1149	100.0	288	21	AAW99966	Human B7 protein.
7	1149	100.0	288	21	AAW44289	Human B7.1 co-stim
8	1149	100.0	288	21	AAW54920	Human B7.1 protein
9	1149	100.0	288	22	AAU05121	Colorectal tumour
10	1149	100.0	288	22	AAW19959	Human B lymphocyte

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1149	100.0	288	16	AAR67989	Human B lymphocyte
2	1149	100.0	288	18	AAW38414	B7-1. Homo sapien
3	1149	100.0	288	20	AAW67804	Human B7 protein s
4	1149	100.0	288	20	AAW73640	Human B7-2 antigen
5	1149	100.0	288	21	AAW37087	Human B lymphocyte
6	1149	100.0	288	21	AAW99966	Human B7 protein.
7	1149	100.0	288	21	AAW44289	Human B7.1 co-stim
8	1149	100.0	288	21	AAW54920	Human B7.1 protein
9	1149	100.0	288	22	AAU05121	Colorectal tumour
10	1149	100.0	288	22	AAW19959	Human B lymphocyte

11	1149	100.0	288	23	AAE14633	Human B7-1 protein
12	1149	100.0	288	23	AAE15829	Human co-stimulat
13	1149	100.0	288	23	AAW50795	Human B-lymphocyte
14	1149	100.0	473	18	AAW41415	Human B7.1-murine
15	1146	99.7	251	20	AAW90208	hB7.IgIU-glu solub
16	1144	99.6	475	18	AAW38415	Soluble B7-1-Ig.
17	1143	99.5	488	20	AAW86004	Human B7-1.5T4.1 p
18	1143	99.5	488	22	AAW83836	Amino acid sequenc
19	1143	99.5	492	19	AAW42338	CD80-Ig-alpha-tp f
20	1138	99.0	480	20	AAW90206	hB7.1FC soluble fu
21	1096	95.4	233	23	AAE15832	Human co-stimulat
22	1047	91.1	208	18	AAW35858	Human B7.1 for use
23	761	66.2	229	22	AAW97780	Soluble porcine B7
24	761	66.2	229	23	AAE15831	Pig co-stimulatory
25	743	64.7	292	21	AAW32283	Feline CD80 (B7-1)
26	743	64.7	292	21	AAW32276	Feline CD80 (B7-1)
27	743	64.7	292	23	AAO17732	Feline CD80 (B7-1)-TA
28	743	64.7	292	23	AAU78119	Feline CD80 (TAMU)
29	739	64.3	292	21	AAW32284	Feline CD80 (B7-1)
30	739	64.3	292	21	AAW32277	Feline CD80 (B7-1)
31	739	64.3	292	23	AAO17733	Feline CD80 (SYNTR
32	739	64.3	292	23	AAU78120	Feline CD80 (SYNTR
33	719	62.6	304	20	AAW41075	Canine B7-1 protei
34	705	61.4	235	20	AAW41077	Canine B7-1S prote
35	561	48.8	306	16	AAW82893	Mouse B7-1 alterna
36	561	48.8	306	16	AAW67990	Murine B lymphocy
37	561	48.8	306	22	AAW19960	Mouse B lymphocyte
38	561	48.8	306	23	AAU99783	T-cell costimulat
39	561	48.8	306	23	AAW50796	Mouse B-lymphocyte
40	561	48.8	320	16	AAW82892	Mouse B7-1 alterna
41	558	48.6	306	20	AAW67805	Mouse B7 protein s
42	558	48.6	306	20	AAW73641	Mouse B7-2 antigen
43	558	48.6	306	21	AAW37088	Murine B lymphocy
44	558	48.6	306	21	AAW99967	Murine B7 protein.
45	467.5	40.7	631	23	AAU75547	Rat B7-like protei

ALIGNMENTS

RESULT 1
AAR67989
ID AAR67989 standard; Protein; 288 AA.
XX
AC AAR67989;
XX
DT 21-AUG-1995 (first entry)
XX
DE Human B lymphocyte antigen B7-1 (hB7-1).
XX
KW B lymphocyte antigen; B7-1; B cell activation antigen; CD28;
KW ligand; T cell surface antigen; transmembrane protein.
XX
OS Homo sapiens.
XX
FH Key
FT Protein
FT Location/Qualifiers
FT 1..34
FT /label= signal sequence
FT /note= "hydrophobic"
FT 35..242
FT /label= extracellular
FT 243..269
FT /label= transmembrane
FT 270..288
FT /label= intracellular
FT Misc-difference 53..55
FT /label= N-linked glycosylation
FT Misc-difference 89..91
FT /label= see above
FT Misc-difference 98..100
FT /label= see above
FT Misc-difference 186..188
FT /label= see above

FT Misc-difference 207..209
 FT /label= see above
 FT Misc-difference 211..213
 FT /label= see above
 FT Misc-difference 226..228
 FT /label= see above
 FT Misc-difference 232..234
 FT /label= see above
 FT Domain
 FT 35..138
 FT /label= Ig V-set domain
 FT Domain
 FT 139..236
 FT /label= Ig C-set domain
 FT XX
 FN WO9503408-A.
 XX 02-FEB-1995.
 PD 26-JUL-1994; 94WO-US08423.
 XX 26-JUL-1993; 93US-0101624.
 PR 19-AUG-1993; 93US-0109393.
 PR 03-NOV-1993; 93US-0147773.
 XX (DAND) DANA FARBER CANCER INST INC.
 PA (REPK) REPLIGEN CORP.
 XX Freeman GJ, Gray GS, Greenfield E, Nadler LM;
 PI WPI; 1995-075236/10.
 DR N-PSDB; AAQ81371.
 XX Nucleic acids encoding CTLA4/CD28 counter receptor, B7-2 - useful
 PT for enhancing or suppressing T-cell mediated immune responses
 FT
 XX Disclosure; pages 111-113; 175pp; English.
 PS Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,
 CC cell line Raji, clone no. 13. Its position in the genome is
 CC chromosome/segment 3. It was published by Freeman, F.J. et al.,
 CC J. of Immunology, 143: 8: 2714-2722, 15th October 1989. It can be
 CC found in Genbank at Accession no. M27533. The encoded protein,
 CC R67989, binds both human CTLA4 and human CD28. It is related
 CC to human hb7-2 (see Q81351) and murine hb7 (see Q81372).
 XX
 XX Sequence 288 AA;
 SQ
 Query Match 100.0%; Score 1149; DB 16; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKQKMKVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKQKMKVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
 DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
 QY 181 NMTTNHSMCLIKYGLHVRNQTFFNNWTTKQEHFPDN 216
 DB 207 NMTTNHSMCLIKYGLHVRNQTFFNNWTTKQEHFPDN 242
 RESULT 2
 ID AAW38414
 XX AAW38414 standard; Protein; 288 AA.
 AC AAW38414;
 XX

DT 08-APR-1998 (first entry)
 XX B7-1.
 DE Screening; inhibitor; enhancer; binding; CD28; B7-1.
 XX Screening; inhibitor; enhancer; binding; CD28; B7-1.
 KW Homo sapiens.
 XX EF95554-A2.
 PN 17-SEP-1997.
 PD 04-MAR-1997; 97EP-0301438.
 XX 02-OCT-1996; 96JP-0262085.
 PR 05-MAR-1996; 96JP-0047795.
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA Hattori M, Hida T, Kurokawa T, Nakanishi A;
 XX WPI; 1997-450803/42.
 DR N-PSDB; AAT96358.
 DR New xanthene derivatives useful as immunomodulators - e.g. methyl
 XX 2-(carboxymethylsulphonyl)-5,7-dichloro-3,8-dihydroxy-6-
 PT methyl-9-oxo-9H-xanthene-1-carboxylate.
 PT Disclosure; Fig 4; 117pp; English.
 PS The present sequence was used in the development of a novel method
 XX for screening for compounds that inhibit or enhance binding of CD28
 CC to B7-1.
 CC
 XX Sequence 288 AA;
 SQ
 Query Match 100.0%; Score 1149; DB 18; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKQKMKVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKQKMKVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
 DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
 QY 181 NMTTNHSMCLIKYGLHVRNQTFFNNWTTKQEHFPDN 216
 DB 207 NMTTNHSMCLIKYGLHVRNQTFFNNWTTKQEHFPDN 242
 RESULT 3
 ID AAW67804
 XX AAW67804 standard; Protein; 288 AA.
 AC AAW67804;
 XX 13-APR-1999 (first entry)
 DT Human B7 protein sequence.
 XX Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;
 KW T-cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH

Peptide 1..34
 FT /note= "signal peptide"
 FT Protein 35..288
 FT /note= "mature B7 protein"
 FT Domain 35..242
 FT /note= "extracellular domain"
 FT Domain 243..269
 FT /note= "transmembrane domain"
 FT Domain 270..288
 FT /note= "intracellular domain"
 FT Modified-site 53..55
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 89..91
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 98..100
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 186..188
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 207..209
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 211..213
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 226..228
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 236..234
 FT /note= "Asn is N-glycosylated"
 FT Domain 35..139
 FT /note= "Ig V-set domain"
 FT Domain 140..236
 FT /note= "Ig C-set domain"
 XX
 XX US5858776-A.
 XX
 XX 12-JAN-1999.
 XX
 XX 03-NOV-1993; 93US-0147772.
 XX
 XX 03-NOV-1993; 93US-0147772.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 XX (HARD) HARVARD COLLEGE.
 XX (REFK) REPLIGEN CORP.
 XX
 XX Baskar S, Freeman GJ, Glimcher LH, Nadler LM, Ostrand-Rosenberg S;
 XX WPI: 1999-119893/10.
 XX N-PSDB; AAX00757.
 XX
 XX New modified tumour cells - transfected in order to express a T cell
 FT costimulatory molecule which allows the induction of an anti-tumour
 FT response by T cells
 FT
 XX Disclosure; Column 31-34; 24pp; English.

XX This sequence represents the amino acid sequence of a human B7 protein.
 CC The coding sequence can be used to transfect mammalian tumour (sarcoma)
 CC cell so that the B7 protein is expressed by the tumour cell and has the
 CC ability to co-stimulate T cells and bind CD28 or CTLA4 ligand.
 CC The modified tumour cells can be used for inducing an anti-tumour
 CC T-lymphocyte response in a subject and are effective against both
 CC modified and unmodified tumour cells. The modified tumour cells can
 CC also be administered to prevent or inhibit metastatic spread of a tumour
 CC or to prevent or inhibit recurrence of a tumour following therapeutic
 CC treatment.
 XX
 XX Sequence 288 AA;
 XX
 XX Query Match 100.0%; Score 1149; DB 20; Length 288;
 XX Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 XX Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 86
 QY 61 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVSVKADFPPTS 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 87 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVSVKADFPPTS 146

Db 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 86
 QY 61 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVSVKADFPPTS 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 87 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVSVKADFPPTS 146
 QY 121 ISDPEIPTSNIIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 147 ISDPEIPTSNIIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
 QY 181 NMTNHSFMCLIKYGHRLRVNQTENNTTKQEHFPDN 216
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 207 NMTNHSFMCLIKYGHRLRVNQTENNTTKQEHFPDN 242

RESULT 4
 AAW73640
 ID AAW73640 standard; Protein; 288 AA.
 XX AC AAW73640;
 XX DT 23-MAR-1999 (first entry)
 XX DE Human B7-2 antigen.
 XX KW B7-2 antigen; mammalian tumour cell; T cell costimulation; CD28 ligand;
 KW CTLA4 ligand; therapy; T-cell response; human.
 XX OS Homo sapiens.
 XX PN US5861310-A.
 XX PD 19-JAN-1999.
 XX PF 30-MAY-1995; 95US-0456104.
 XX PR 30-MAY-1995; 95US-0456104.
 XX PR 03-NOV-1993; 93US-0147773.
 XX (DAND) DANA FARBER CANCER INST INC.
 XX PI Freeman GJ, Gray GS, Nadler LM;
 XX WPI: 1999-130394/11.
 XX N-PSDB; AAV55786.
 XX Tumour cell transfected to express B7-2 molecule - useful for tumour
 FT therapy by stimulating T-cell response
 FT
 XX Disclosure; Column 37-40; 27pp; English.

XX This sequence is the human B7-2 antigen, which can be used in the
 CC method of the invention. The method is for transfecting an isolated
 CC mammalian tumour cell with an exogenous nucleic acid molecule encoding a
 CC mammalian B7-2 molecule, where the B7-2 molecule is expressed in the
 CC tumour cell is capable of costimulating a T cell and is capable of
 CC binding a CD28 or CTLA4 ligand. The method is useful for treating tumours
 CC by stimulating a T-cell response against tumour cells in vivo.

XX Sequence 288 AA;
 XX
 XX Query Match 100.0%; Score 1149; DB 20; Length 288;
 XX Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 XX Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 86
 QY 61 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVSVKADFPPTS 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 87 YKNTTFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVSVKADFPPTS 146

QY 121 ISDFEIPSNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 180
 Db 147 ISDFEIPSNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 206
 QY 181 NMTNHSFMCILIKYGHRLVNOTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGHRLVNOTFNWNTTKQEHFPDN 242

RESULT 5

AAB37087
 ID AAB37087 standard; Protein; 288 AA.
 AC AAB37087;
 DT 28-MAR-2001 (first entry)
 DE Human B lymphocyte antigen B7-1.
 KW Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;
 KW antigen; extracellular domain; CTLA4; immunoglobulin constant region;
 KW immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;
 KW T cell-mediated immune response; transplantation; vaccination.
 XX Homo sapiens.
 OS US6130316-A.
 PN 10-OCT-2000.
 PD 26-JUL-1994; 94US-0280757.
 PR 26-JUL-1993; 93US-0101624.
 PR 19-AUG-1993; 93US-0109393.
 PR 03-NOV-1993; 93US-0147773.
 XX (DAND) DANA FARBER CANCER INST INC.
 PA (REPK) REPLIGEN CORP.
 PI Freeman GJ, Nadler LM, Gray GS, Greenfield E;
 DR WPI; 2000-655681/63.
 DR N-PSDB; AAC84051.

Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for enhancing or suppressing T cell-mediated immune responses, especially during tissue, skin or organ transplantation, or in graft-versus-host disease

Disclosure; Column 87-90; 83pp; English.

PS The invention relates to an isolated nucleic acid molecule encoding a
 CC fusion protein comprising a first nucleotide sequence encoding a first
 CC peptide, and a second nucleotide sequence encoding a second peptide.
 CC The first nucleotide sequence hybridizes in 6 x sodium chloride/sodium
 CC citrate (SSC) at 45 deg. C, followed by a wash in 0.2 x SSC at 50 deg. C
 CC to a portion of a nucleotide sequence which encodes a human or murine
 CC B lymphocyte antigen (B7-2) extracellular domain. The first peptide has
 CC the ability to bind CD28 or CTLA4. The first peptide has an amino acid
 CC sequence that is identical or at least 50% identical with the
 CC extracellular domain of a human B7-2 peptide (AAB37085). The second
 CC peptide is especially an immunoglobulin constant region. This sequence
 CC represents the human B lymphocyte antigen B7-1. The sequence is used for
 CC comparison with the B7-2 sequence. The human B7-2 protein is an example
 CC of a first peptide sequence of the invention. The nucleic acid molecules
 CC are useful in various expression vectors to direct synthesis of the
 CC corresponding proteins or peptides in a variety of hosts, particularly
 CC eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic
 CC acids are also useful for enhancing the immunogenicity of a mammalian
 CC cell, e.g. tumour cell (sarcoma) or an antigen presenting cell
 CC (macrophage). The fusion proteins or peptides are useful for enhancing or
 CC suppressing T cell-mediated immune responses, e.g. in situations of
 CC tissue, skin or organ transplantation, or in graft-versus-host disease.

CC The proteins are also useful for enhancing the efficacy of vaccination
 CC against a variety of pathogens, and may also be used to upregulate an
 CC immune response against a particular pathogen during an infection or
 CC against a tumour in a tumour-bearing host.

XX Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSGCHNVSVLELAQTRIYWQEKKKVLTMMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEVATLSGCHNVSVLELAQTRIYWQEKKKVLTMMSGDMNIWPE 86
 QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVLYEKDAFKREHLAEVTLVSKADFPPTS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVLYEKDAFKREHLAEVTLVSKADFPPTS 146
 QY 121 ISDFEIPSNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 180
 Db 147 ISDFEIPSNIRRIICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 206
 QY 181 NMTNHSFMCILIKYGHRLVNOTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGHRLVNOTFNWNTTKQEHFPDN 242

RESULT 6

AAY99966
 ID AAY99966 standard; Protein; 288 AA.

XX AAY99966;

DT 10-JAN-2001 (first entry)

XX Human B7 protein.

DE B7; human; B cell activation antigen; B lymphocytes;
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
 KW herpes simplex; influenza; common cold; HIV.

XX Homo sapiens.

Key	Location/Qualifiers
Peptide	1..34
Domain	/label= signal_peptide
Domain	35..242
Domain	/label= Extracellular_domain
Domain	35..138
Modified-site	/label= "Ig V-set domain"
Modified-site	53..55
Modified-site	/note= "N-linked glycosylation site"
Modified-site	89..91
Modified-site	/note= "N-linked glycosylation site"
Domain	98..100
Domain	/note= "N-linked glycosylation site"
Domain	139..236
Domain	/label= "Ig C-set domain"
Modified-site	186..188
Modified-site	/note= "N-linked glycosylation site"
Modified-site	207..209
Modified-site	/note= "N-linked glycosylation site"
Modified-site	211..213
Modified-site	/note= "N-linked glycosylation site"
Modified-site	226..228
Modified-site	/note= "N-linked glycosylation site"
Modified-site	232..234
Modified-site	/note= "N-linked glycosylation site"
Domain	243..269
Domain	/label= Transmembrane_domain
Domain	270..288
Domain	/label= Intracellular_domain

XX US6071716-A.
 XX 06-JUN-2000.
 XX 15-NOV-1993; 93US-0153262.
 XX 28-AUG-1991; 91US-0751306.
 XX 01-OCT-1990; 90US-0591300.
 XX (DAND) DANA FARBER CANCER INST INC.
 XX Nadler LM, Freeman GJ, Freedman AS;
 XX WPI: 2000-422081/36.
 XX N-PSDB; AA61328.
 XX New polynucleotides encoding a B7 activation antigen, useful for
 PT regulating T cell mediated immune responses or viral diseases -
 XX
 XX Claim 1; Fig 4; 36pp; English.
 XX The present sequence is the unique human B cell activation antigen B7
 CC protein. The cDNA encoding this sequence was isolated from a Burkitt
 CC lymphoma cell line cDNA library. Selection of cDNA clones was based
 CC on expression of B7, as detected by the anti-B7 monoclonal antibody.
 CC The human B7 cDNA was used in hybridisation analysis to isolate the
 CC murine B7 cDNA (see AAA61329). The B7 nucleic acid sequences may be
 CC used to generate transgenic, knock-out animals which, in turn, are
 CC useful in the development and screening of therapeutically useful
 CC reagents. The expressed B7 protein is useful for enhancing or
 CC blocking activated T cell mediated immune responses and immune
 CC function. Modification of B7 expression is useful in the treatment of
 CC autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis),
 CC herpes simplex, influenza, the common cold and HIV. It is also useful
 CC in tissue and organ transplantation.
 XX
 SQ Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVLELAQRIYQKEKKMVLTMGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVLELAQRIYQKEKKMVLTMGDMNIWPE 86
 QY 61 YKNRTIFDTNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADPPTPS 120
 DB 87 YKNRTIFDTNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADPPTPS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
 QY 181 NMTNHSFMCILIKYGLHRLVNTQFNWNTTKQEHFPDN 216
 DB 207 NMTNHSFMCILIKYGLHRLVNTQFNWNTTKQEHFPDN 242
 RESULT 7
 AAY44289
 ID AAY44289 standard; Protein; 288 AA.
 XX AAY44289;
 XX 29-FEB-2000 (first entry)
 XX Human B7.1 co-stimulatory molecule.
 XX Human B7.1 co-stimulatory molecule; antigen presenting cell;
 KW immune response; cell surface receptor; Major histocompatibility complex;
 KW MHC classII; proton motor force; mitochondrial membrane potential;

KW mitochondrial metabolism; cancer; autoimmune disease; glycoprotein;
 KW neurodegenerative disorder.
 XX Homo sapiens.
 XX WO9593953-A2.
 XX 28-OCT-1999.
 XX 30-MAR-1999; 99WO-US06874.
 XX 17-APR-1998; 98US-0082250.
 XX 29-JUL-1998; 98US-0094519.
 XX 24-SEP-1998; 98US-0101580.
 XX (UYVE-) UNIV VERMONT.
 XX Newell MK;
 XX WPI: 2000-096773/08.
 XX N-PSDB; AA29320.
 XX Use of cell surface and membrane characteristics for developing
 PT products for treating cancers, autoimmune diseases or neurodegenerative
 PT diseases -
 XX
 XX Disclosure; Page 115; 123pp; English.
 XX The present sequence is human B7.1 co-stimulatory molecule. This is
 CC a glycoprotein on the surface of antigen presenting cells. This is
 CC involved in stimulation of an immune response by its ability to interact
 CC with various immune cell surface receptors. The regulation of cell
 CC surface expression of MHC classII and co-stimulatory molecule B7 can be
 CC manipulated by regulating the intracellular dissipation of proton motor
 CC force which can be assessed in terms of mitochondrial membrane potential.
 CC These methods can be used for regulating cell growth and division to
 CC control disease processes by manipulating mitochondrial metabolism and
 CC the expression of cell surface immune proteins. They can be used for
 CC treating diseases associated with excessive cellular division, aberrant
 CC differentiation, and premature cellular death, e.g. cancers, autoimmune
 CC diseases, neurodegenerative disorders etc.
 XX
 SQ Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVLELAQRIYQKEKKMVLTMGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVLELAQRIYQKEKKMVLTMGDMNIWPE 86
 QY 61 YKNRTIFDTNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADPPTPS 120
 DB 87 YKNRTIFDTNNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADPPTPS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
 QY 181 NMTNHSFMCILIKYGLHRLVNTQFNWNTTKQEHFPDN 216
 DB 207 NMTNHSFMCILIKYGLHRLVNTQFNWNTTKQEHFPDN 242
 RESULT 8
 AAY54920
 ID AAY54920 standard; Protein; 288 AA.
 XX AAY54920;
 XX 14-FEB-2000 (first entry)
 XX

DE Human B7.1 protein sequence.
 KW Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
 KW IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.
 XX
 OS Homo sapiens.
 XX
 PN US5994104-A.
 XX
 PD 30-NOV-1999.
 XX
 PF 08-NOV-1996; 96US-0751767.
 XX
 PR 08-NOV-1996; 96US-0751767.
 XX
 PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
 XX
 PI Anderson RJ, Prentice HG, MacDonald ID;
 XX
 DR WPI; 2000-038261/03.
 DR N-PSDB; AAZ40022.
 XX
 PT Nucleic acid constructs encoding interleukin-12 fusion proteins useful
 PT for treating leukemia and other cancers -
 XX
 PS Example; Fig 10; 73pp; English.
 XX
 CC This sequence represents the human B7.1 protein sequence.
 CC The invention relates to an isolated nucleic acid construct (I)
 CC comprising a region encoding an interleukin-12 (IL-12) fusion protein
 CC comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker
 CC peptide (joining the subunits) and a region encoding a B7 protein. (I)
 CC may be used to produce IL-12 fusion proteins according to standard
 CC recombinant DNA methodologies. The fusion proteins may be produced either
 CC in vitro in a fermentation culture or in vivo as part of a gene therapy
 CC protocol (in this case (I) is used to transform a patients cells, which
 CC then secrete the functional polypeptide to supplement the patients own
 CC production of IL-12 or to rectify mutations which lead to the expression
 CC of inactive polypeptides). The fusion proteins produced in this way may
 CC be used to treat any disease which responds to IL-12 such as tumours
 CC (both solid and dispersed of the kidney, breast, colon, ovarian and
 CC cervical tumours and melanomas) and in particular, tumours of the blood
 CC such as leukaemia. Alternatively, the polypeptides may be used as
 CC antigens in the production of antibodies to IL-12 and to assay for
 CC agonists and antagonists of its activity. The antibodies and antagonists
 CC may be used to inhibit the activity of IL-12. (I) may also be used
 CC diagnostically as a probe which hybridizes to sequences encoding IL-12
 CC and the antibodies may be used to detect the presence of IL-12
 CC polypeptides in samples. They may be used diagnostically to quantitate
 CC the expression of the polypeptide by patients and hence which subjects
 CC may be in need of restorative therapy.
 XX
 SQ Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCSGVIHVTKEVKVATILSCGHNSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 60
 DB 27 GLSHFCSGVIHVTKEVKVATILSCGHNSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDIF 180
 DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDIF 206
 QY 181 NMTTNHSPCLIKYGHRLRYNQTFNNWTTQEHFPDN 216
 DB 207 NMTTNHSPCLIKYGHRLRYNQTFNNWTTQEHFPDN 242

RESULT 9
 AAU05121
 ID AAU05121 standard; Protein; 288 AA.
 XX
 AC AAU05121;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Colorectal tumour antigen CD80.
 XX
 KW Colorectal cancer; immunostimulant; cytostatic; immune response;
 KW adenocarcinoma; allogeneic tumour cell; SW620 cell; COLO 205 cell;
 KW SW403 cell; colon; breast; lung; prostate; cancer; vaccine;
 KW tumour antigen CD80.
 XX
 OS Homo sapiens.
 XX
 PN WO200154716-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-US02731.
 PR 27-JAN-2000; 2000US-0178498.
 PR 28-FEB-2000; 2000US-0185335.
 XX
 PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Sobol RE, Shawler DL, Bartholomew RM, Carlo DJ, Gold DP;
 XX
 DR WPI; 2001-502616/55.
 DR N-PSDB; AAS11426.
 XX
 PT New composition comprising an allogeneic tumour cell, useful for
 PT stimulating an immune response in a patient having an adenocarcinoma,
 PT especially useful for treating colorectal, breast, lung or prostate
 PT cancer -
 XX
 PS Example 2; Page 130-131; 131pp; English.
 XX
 CC The invention relates to a composition for stimulating an immune response
 CC in a patient having an adenocarcinoma or colorectal cancer. The
 CC composition comprises an allogeneic tumour cell selected from SW620 cell,
 CC COLO 205 cell and SW403 cell, and a physiological carrier. The allogeneic
 CC cell stimulates an immune response to an autologous tumour cell in the
 CC patient. The composition is useful for stimulating an immune response in
 CC a patient having an adenocarcinoma, e.g. colon, breast, lung or prostate
 CC adenocarcinoma. The use of allogeneic tumour cells provides a generic
 CC source of antigen that can be administered to a variety of patients, in
 CC contrast to using autologous tumour cells, which must be isolated from
 CC each individual patient. The allogeneic cells are suitable as a cancer
 CC vaccine and can stimulate an immune response against autologous tumour
 CC cells of a cancer patient. The present sequence represents the amino acid
 CC sequence of colorectal tumour antigen CD80 used in the method of the
 CC invention.
 XX
 SQ Sequence 288 AA;
 Query Match 100.0%; Score 1149; DB 22; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCSGVIHVTKEVKVATILSCGHNSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 60
 DB 27 GLSHFCSGVIHVTKEVKVATILSCGHNSVEELAQTRIYQWKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADFPPTS 146

QY 121 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
 QY 181 NMTNHSFMCCLIKYGLRVNQTNNWTTKQEHFPDN 216
 Db 207 NMTNHSFMCCLIKYGLRVNQTNNWTTKQEHFPDN 242

RESULT 10

AAB19959
 ID AAB19959 standard; Protein; 288 AA.
 XX
 AC AAB19959;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Human B lymphocyte antigen B7.
 KW Human; B7; B lymphocyte; antigen; T cell costimulatory molecule;
 KW CD28; CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;
 KW metastasis; antitumour; therapy.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..34
 FT /label= Signal_peptide
 FT Protein 35..288
 FT /label= Mature_protein
 FT Domain 35..242
 FT /note= "extracellular domain"
 FT Domain 243..269
 FT /note= "transmembrane domain"
 FT Domain 270..288
 FT /note= "intracellular domain"
 FT Domain 35..138
 FT /note= "immunoglobulin V-set domain"
 FT Domain 139..236
 FT /note= "immunoglobulin C-set domain"
 FT Modified-site 53..55
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 89..91
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 98..100
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 186..188
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 207..209
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 211..213
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 226..228
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 232..234
 FT /note= "Asn is N-glycosylated"

XX US6149905-A.

XX 21-NOV-2000.

PF 23-SEP-1998; 98US-0159135.

XX 03-NOV-1993; 93US-0147772.

XX (GENY) GENETICS INST INC.
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (HARD) HARVARD COLLEGE.

XX Baskar S, Glimcher LH, Freeman GJ, Ostrand-Rosenberg S;
 PI Nadler LM;

XX WPI; 2001-079388/09.

DR N-PSDB; AAA89224.

XX Modifying tumor cell for treating tumors, reducing metastatic spread,
 PT inhibiting recurrence of tumor and increasing immunogenicity, involves
 PT transfecting tumor cells with a nucleic acid encoding B7 molecule -
 XX
 PS Claim 4; Column 31-34; 24pp; English.

XX The present sequence is that of human lymphocyte antigen B7, a T
 CC cell costimulatory molecule that binds to CD28 and CTLA4. Tumour
 CC cells modified to express a T cell costimulatory molecule,
 CC especially B7, are disclosed. The tumour cells are modified by
 CC transfection with a nucleic acid encoding the T cell costimulatory
 CC molecule, by using an agent which induces or increases expression
 CC of the T cell costimulatory molecule on the tumour cell surface, or
 CC by coupling the T cell costimulatory molecule to the tumour cell
 CC surface. Tumour cells further modified to express major
 CC histocompatibility complex (MHC) class I and/or class II molecules,
 CC or in which expression of an MHC associated protein, the invariant
 CC chain, is inhibited are also disclosed. The modified tumour cells
 CC are used to treat a patient with a tumour, preventing or inhibiting
 CC metastatic spread or tumour recurrence. The tumour may be a
 CC melanoma, a neuroblastoma, a leukaemia or a carcinoma. A method for
 CC specifically inducing a CD4+ T cell response against a tumour, and a
 CC method for treating a tumour by modification of tumour cells in vivo
 CC are also disclosed. The treatment methods increase the immunogenicity
 CC of the tumour cell in vivo. The antitumour T cell-mediated immune
 CC response is effective both against the modified tumour cells and the
 CC unmodified tumour cells from which the modified cells were derived.
 CC Thus, the effector phase of the antitumour response induced by the
 CC modified tumour cells is not dependent upon expression of a
 CC costimulatory molecule on the tumour cells.

XX Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 22; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSEELAQTRIYQKEKKMYLTMMSGDMNIWPE 60
 |||||

Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSEELAQTRIYQKEKKMYLTMMSGDMNIWPE 86
 |||||

QY 61 YKNTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVSKADFTPS 120
 |||||

Db 87 YKNTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVSKADFTPS 146
 |||||

QY 121 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
 |||||

Db 147 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
 |||||

QY 181 NMTNHSFMCCLIKYGLRVNQTNNWTTKQEHFPDN 216
 |||||

Db 207 NMTNHSFMCCLIKYGLRVNQTNNWTTKQEHFPDN 242
 |||||

RESULT 11

AAE14633
 ID AAE14633 standard; Protein; 288 AA.

XX
 AC AAE14633;

XX 16-JUL-2002 (first entry)

XX Human B7-1 protein.

XX T cell; CD3; accessory molecule; CD28; cancer; infectious disease;
 KW immunotherapy; human immunodeficiency virus; HIV infection;
 KW cytokine; human; B7-1; CD80.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..34
 FT /label= Signal_peptide
 FT Protein 35..288
 FT /note= "Mature B7-1 protein"
 FT Domain 35..242
 FT /label= Extracellular_domain
 FT Domain 35..138
 FT /note= "Ig V-set domain"
 FT Modified-site 53..55
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 89..91
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 98..100
 FT /note= "Asn is N-glycosylated"
 FT Domain 139..236
 FT /note= "Ig C-set domain"
 FT Modified-site 186..188
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 207..209
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 211..213
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 226..228
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 232..234
 FT /note= "Asn is N-glycosylated"
 FT Domain 243..269
 FT /label= Transmembrane_domain
 FT Domain 270..288
 FT /label= Intracellular_domain
 XX USG352694-B1.
 PN
 XX
 XX
 PD
 XX
 PF 10-MAR-1995; 95US-0403253.
 XX
 XX
 PR 03-JUN-1994; 94US-0253964.
 XX
 PA (GENY) GENETICS INST INC.
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;
 XX
 DR WPI; 2002-314696/35.
 DR N-PSDB; AAD27967.
 XX
 PT Inducing T cell population to proliferate, useful in cancer therapy,
 PT comprises activating T cells by contacting T cells in vitro with
 PT immobilized anti-CD3 antibody and stimulating accessory molecule on T
 PT cell surface -
 XX
 XX
 PS Example 11; Column 59-62; 71pp; English.
 XX
 CC The invention relates to a method of inducing T cell population to
 CC proliferate for use in therapy comprising activating T cells by
 CC contacting T cells in vitro with anti-CD3 antibody which is immobilised
 CC on solid phase surface, and stimulating accessory molecule on T cell
 CC surface in vitro with anti-CD28 antibody, or stimulatory form of
 CC natural ligand for CD28 such as B7-1 or B7-2. The method is useful
 CC for inducing a population of T cells to proliferate in sufficient
 CC numbers for use in therapy e.g., for treating cancer or an infectious
 CC disease. The method can be used to selectively expand the
 CC population of CD28⁺, CD4⁺, CD8⁺, CD28RA⁺ or CD28RO⁺ T cells for
 CC immunotherapy. The T cell population resulting by the method can be
 CC genetically transduced and used for immunotherapy or can be used for in
 CC vitro analysis of infectious agents such as human Immunodeficiency
 CC virus (HIV). Proliferation of a population of CD4⁺ T cells obtained
 CC from an individual infected with HIV can be achieved and the cells
 CC rendered resistant to HIV infection. Following the expansion of the T
 CC cells to sufficient numbers, the expanded T cells are restored to the
 CC individual. Also CD4⁺ T cells expanded by the above mentioned is
 CC useful for treating HIV infection in an individual. A population

CC of tumour-infiltrating lymphocytes can be obtained from an individual
 CC afflicted with cancer and the T cells stimulated to proliferate to
 CC sufficient numbers and restored to the individual. The supernatants from
 CC cultures of T cells expanded from above mentioned method are useful as a
 CC rich source of cytokines and can be used to sustain T cells in vivo or
 CC ex vivo. Stimulating and expanding a population of antigen specific
 CC T cells are useful in therapeutic conditions where it is desirable to
 CC upregulate an immune response. The T cell proliferation occurs in
 CC the absence of exogenous growth factors or accessory cells. The present
 CC sequence is human B7-1 (CD80) transmembrane protein used in the
 CC invention.

XX SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKEVATLSGHNVSVEELATRIYVQKEKKMLVTMMSGDMNIWPE 60
 DB 27 GLSHFCSGVIHVTKEVKEVATLSGHNVSVEELATRIYVQKEKKMLVTMMSGDMNIWPE 86
 QY 61 YKNETIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLVKADPPTPS 120
 DB 87 YKNETIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLVKADPPTPS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLDLF 180
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLDLF 206
 QY 181 NMTTNHSEFMCLIKYGHRLVNTQTFNNTTKQEHFPDN 216
 DB 207 NMTTNHSEFMCLIKYGHRLVNTQTFNNTTKQEHFPDN 242

RESULT 12

AAE15829
 ID AAE15829 standard; Protein; 288 AA.

XX AAE15829;

XX AC
 XX 26-MAR-2002 (first entry)

XX Human co-stimulatory molecule, B7-1 protein.

XX Human; vaccine; immunostimulatory molecule; interferon; IFN; therapy;
 KW antigen presentation; vaccine; tumourigenesis; cancer; cytostatic;
 KW antitumour; antibacterial; virucide; fungicide; protozoacide; B7-1.

XX Homo sapiens.

XX WO200188097-A1.

XX PN
 XX 22-NOV-2001.

XX PF 17-MAY-2001; 2001WO-AU00565.

XX PR 17-MAY-2000; 2000AU-0007553.

XX PA (MONU) UNIV MONASH.

XX PI Ralph SJ;

XX WPI; 2002-082990/11.

XX DR N-PSDB; AAD25509.

XX New composition, useful for treatment and/or prophylaxis of cancer and
 PT tumor, comprises immunostimulatory molecule and animal cells cultured
 PT in presence of interferon to enhance antigen presenting function of the
 PT cells -

XX Claim 6; Page 99-100; 127pp; English.

XX

CC The present invention relates to a composition of matter comprising an
 CC immunostimulatory molecule and animal cells cultured in the presence of
 CC at least one interferon (IFN) for a time and under conditions sufficient
 CC to enhance the antigen presenting function of the cells. The invention
 CC is used as vaccine. The composition is useful for treatment and/or
 CC prophylaxis of tumorigenesis, cancer, viral, bacterial, fungal and
 CC protozoal infections. The composition which comprises the soluble
 CC immunostimulatory molecule and the cultured animal cells is administered
 CC separately, sequentially or simultaneously to the patient. The present
 CC sequence is human co-stimulatory molecule, B7-1 protein.

XX Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKWKVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKWKVLTMMSGDMNIWPE 86
 QY 61 YKNTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVKADFPPTPS 120
 DB 87 YKNTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVKADFPPTPS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLNINNTVSDPETELIYAVSSKLDLF 180
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLNINNTVSDPETELIYAVSSKLDLF 206
 QY 181 NMTNHSFMCILIKYGLHRLVNTQFNWNTTQKQHFDPN 216
 DB 207 NMTNHSFMCILIKYGLHRLVNTQFNWNTTQKQHFDPN 242

RESULT 13

AAM50795

ID AAM50795 standard; Protein; 288 AA.

XX AC AAM50795;

XX 23-APR-2002 (first entry)

XX Human B-lymphocyte antigen B7.

XX B-lymphocyte antigen B7; human; T-cell costimulatory molecule;
 KW tumour; sarcoma; lymphoma; melanoma; neuroblastoma; leukaemia;
 KW carcinoma; cancer; metastasis; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..34
 FT /label= Signal_peptide
 FT Protein 35..288
 FT /label= Mature_protein
 FT Domain 35..242
 FT /label= Extracellular_domain
 FT Domain 243..269
 FT /label= Transmembrane_domain
 FT Domain 270..288
 FT /label= Intracellular_domain
 FT Domain 35..138
 FT /label= Ig_V-set_domain
 FT Domain 139..236
 FT /label= Ig_C-set_domain
 FT Modified-site 53..55
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 89..91
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 98..100
 FT /note= "Asn is N-glycosylated"
 FT Modified-site 186..188
 FT /note= "Asn is N-glycosylated"

Modified-site 207..209
 /note= "Asn is N-glycosylated"
 Modified-site 211..213
 /note= "Asn is N-glycosylated"
 Modified-site 226..228
 /note= "Asn is N-glycosylated"
 Modified-site 232..234
 /note= "Asn is N-glycosylated"

US6319709-B1.

PN 20-NOV-2001.

XX 29-NOV-1999; 99US-0450798.

XX 03-NOV-1993; 93US-0147772.

PR 23-SEP-1998; 98US-0159135.

XX (HARD) HARVARD COLLEGE.

PA (DAND) DANA FARBER CANCER INST INC.

PA (UYMA-) UNIV MARYLAND BALTIMORE COUNTY.

PI Ostrand-Rosenberg S, Baskar S, Glimcher LH, Freeman GJ, Nadler LM;

DR WPI: 2002-138256/18.

DR N-PSDB; ABA91632.

XX An isolated mammalian tumour cell transfected with an exogenous nucleic
 PT acid molecule encoding a mammalian B7 molecule which can be used in
 PT methods for treating a patient with a tumour and preventing or
 PT inhibiting metastatic growth -

PS Claim 2; Column 31-34; 24pp; English.

XX The present sequence is that of human B-lymphocyte antigen B7, a
 CC member of the immunoglobulin superfamily with unique expression on
 CC activated and neoplastic cells. The invention provides tumour
 CC cells modified to express a T-cell costimulatory molecule, such as
 CC a CD28 and/or CTLA4 ligand, preferably B-lymphocyte antigen B7.
 CC The tumour cells are modified by transfection with nucleic acid
 CC encoding the T-cell costimulatory molecule, by using an agent which
 CC induces or increases expression of a T-cell costimulatory molecule
 CC on the tumour cell surface or by coupling a T-cell costimulatory
 CC molecule to the tumour cell surface. The tumour cells may be
 CC further modified to express major histocompatibility complex (MHC)
 CC class I and/or class II molecules or have an MHC associated protein,
 CC the invariant chain, inhibited. The modified tumour cells are used
 CC to treat a patient with a tumour, preventing or inhibiting
 CC metastatic spread of a tumour, preventing or inhibiting
 CC recurrence of a tumour. Modification of tumour cells in vivo
 CC makes them capable of triggering a costimulatory signal in T-cells.
 CC The tumour cell is preferably a sarcoma, lymphoma, melanoma,
 CC neuroblastoma, leukaemia or carcinoma.

XX Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.2e-103;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKWKVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKWKVLTMMSGDMNIWPE 86
 QY 61 YKNTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVKADFPPTPS 120
 DB 87 YKNTIFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLVKADFPPTPS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLNINNTVSDPETELIYAVSSKLDLF 180
 DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLNINNTVSDPETELIYAVSSKLDLF 206
 QY 181 NMTNHSFMCILIKYGLHRLVNTQFNWNTTQKQHFDPN 216

Db 207 NMTNHSFMCILIKYGLHVRNQTFFNNWTTKQEHFPDN 242
|||||

RESULT 14

AAW41415

ID AAW41415 standard; Protein; 473 AA.

XX AC

XX AAW41415;

XX DT

XX 02-JUN-1998 (first entry)

XX DE

XX Human B7.1-murine A5B7 F(ab')₂ fusion protein.

XX KW

XX Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;

XX KW

XX cancer diagnosis; complementarity determining region.

XX OS

XX Chimeric - Homo sapiens.

XX OS

XX Chimeric - Mus sp.

XX PN

XX WO9742329-A1;

XX PD

XX 13-NOV-1997.

XX PF

XX 29-APR-1997; 97WO-GB01165.

XX XX

XX 14-FEB-1997; 97GB-0003103.

XX PR

XX 04-MAY-1996; 96GB-0009405.

XX XX

XX (ZENE) ZENECA LTD.

XX PI

XX Copley CG, Edge MD, Emery SC;

XX DR

XX WPI; 1997-558987/51.

XX DR

XX N-PSDB; AAV17340.

XX PT

XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for

XX PT

XX diagnosis and therapy of cancer

XX PS

XX Reference Example 3; Page 190-193; 208pp; English.

XX CC

XX This sequence is the human B7.1-murine A5B7 F(ab')₂ fusion protein

XX CC

XX (A5B7), and is an example of the antibody of the invention. The antibody

XX CC

XX is an anti-CEA (carcinoembryonic antigen) antibody (preferably

XX CC

XX 806.077 Ab). Host cells or transgenic organisms transformed with DNA

XX CC

XX encoding the antibody, are used to make the antibody or conjugate. The

XX CC

XX conjugate is used in a medicament suitable for intravenous

XX CC

XX administration. The conjugate can be used for cancer therapy, selectively

XX CC

XX killing tumour cells. The antibody can be used for in vivo or in vitro

XX CC

XX diagnosis of cancer.

XX XX

XX Sequence 473 AA;

XX SQ

XX Query Match

XX Best Local Similarity 100.0%; Score 1149; DB 18; Length 473;

XX Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY

XX 1 GLSHFCSGVTHVTKVEKAVATLSGHNVSVEELAQTRIVYQKEKKVLTMTSGDMNIWPE 60

XX Db

XX 27 GLSHFCSGVTHVTKVEKAVATLSGHNVSVEELAQTRIVYQKEKKVLTMTSGDMNIWPE 86

XX QY

XX 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTPS 120

XX Db

XX 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTPS 146

XX QY

XX 121 ISDFEITSNIRRICSTSGGFPFPHLSWLENGELNAINTVSODPETELYAVSSKLDF 180

XX Db

XX 147 ISDFEITSNIRRICSTSGGFPFPHLSWLENGELNAINTVSODPETELYAVSSKLDF 206

Db 207 NMTNHSFMCILIKYGLHVRNQTFFNNWTTKQEHFPDN 242
|||||

RESULT 14

AAW41415

ID AAW41415 standard; Protein; 473 AA.

XX AC

XX AAW41415;

XX DT

XX 02-JUN-1998 (first entry)

XX DE

XX Human B7.1-murine A5B7 F(ab')₂ fusion protein.

XX KW

XX Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;

XX KW

XX cancer diagnosis; complementarity determining region.

XX OS

XX Chimeric - Homo sapiens.

XX OS

XX Chimeric - Mus sp.

XX PN

XX WO9742329-A1;

XX PD

XX 13-NOV-1997.

XX PF

XX 29-APR-1997; 97WO-GB01165.

XX XX

XX 14-FEB-1997; 97GB-0003103.

XX PR

XX 04-MAY-1996; 96GB-0009405.

XX XX

XX (ZENE) ZENECA LTD.

XX PI

XX Copley CG, Edge MD, Emery SC;

XX DR

XX WPI; 1997-558987/51.

XX DR

XX N-PSDB; AAV17340.

XX PT

XX Anti-carcinoembryonic antigen antibody 806.077 Ab - used for

XX PT

XX diagnosis and therapy of cancer

XX PS

XX Reference Example 3; Page 190-193; 208pp; English.

XX CC

XX This sequence is the human B7.1-murine A5B7 F(ab')₂ fusion protein

XX CC

XX (A5B7), and is an example of the antibody of the invention. The antibody

XX CC

XX is an anti-CEA (carcinoembryonic antigen) antibody (preferably

XX CC

XX 806.077 Ab). Host cells or transgenic organisms transformed with DNA

XX CC

XX encoding the antibody, are used to make the antibody or conjugate. The

XX CC

XX conjugate is used in a medicament suitable for intravenous

XX CC

XX administration. The conjugate can be used for cancer therapy, selectively

XX CC

XX killing tumour cells. The antibody can be used for in vivo or in vitro

XX CC

XX diagnosis of cancer.

XX XX

XX Sequence 473 AA;

XX SQ

XX Query Match

XX Best Local Similarity 100.0%; Score 1149; DB 18; Length 473;

XX Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY

XX 1 GLSHFCSGVTHVTKVEKAVATLSGHNVSVEELAQTRIVYQKEKKVLTMTSGDMNIWPE 60

XX Db

XX 27 GLSHFCSGVTHVTKVEKAVATLSGHNVSVEELAQTRIVYQKEKKVLTMTSGDMNIWPE 86

XX QY

XX 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTPS 120

XX Db

XX 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVSKADFPPTPS 146

XX QY

XX 121 ISDFEITSNIRRICSTSGGFPFPHLSWLENGELNAINTVSODPETELYAVSSKLDF 180

XX Db

XX 147 ISDFEITSNIRRICSTSGGFPFPHLSWLENGELNAINTVSODPETELYAVSSKLDF 206

RESULT 15

AAW90208

ID AAW90208 standard; Protein; 251 AA.

XX AC

XX AAW90208;

XX DT

XX 10-MAY-1999 (first entry)

XX DE

XX hb7.lglu-glu soluble fusion protein.

XX XX

XX B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2;

XX KW

XX CD86; T cell activation; inhibitor; graft versus host disease;

XX KW

XX transplant rejection; allograft rejection; autoimmune disease;

XX KW

XX allergy; therapy; human; hb7.lglu-glu.

XX OS

XX Chimeric - Homo sapiens.

XX OS

XX Chimeric - synthetic.

XX XX

XX Key Location/Qualifiers

XX FT

XX Peptide 1..34

XX FT

XX /note= "potential eukaryotic secretory signal

XX FT

XX Peptide" 35..242

XX FT

XX /note= "human B7.1 (mature protein) extracellular

XX FT

XX Peptide 243..251

XX FT

XX /note= "Glu-Glu detection/purification tag"

XX PN

XX WO9858965-A2.

XX XX

XX 30-DEC-1998.

XX XX

XX 22-JUN-1998; 98WO-EP03791.

XX PF

XX 20-JUN-1997; 97EP-0870092.

XX XX

XX (INNO-) INNOGENETICS NV.

XX XX

XX Bosman A, Buyse M, Lorre K, Sablon E;

XX PI

XX WPI; 1999-105615/09.

XX DR

XX New molecules which bind B7.1 and B7.2 - useful to prevent and treat

XX CC

XX immune diseases including allograft rejection

XX PT

XX Example 3.1.2; Fig 4; 182pp; English.

XX PS

XX This 29 kDa soluble fusion protein, termed hb7.lglu-glu, is composed

XX CC

XX of human co-stimulatory molecule B7.1 extracellular domain fused

XX CC

XX C-terminally to a synthetic Glu-Glu epitope (see AAW90197). It

XX CC

XX was produced from total RNA of Epstein-Barr virus-transformed

XX CC

XX human spleen cells by RT-PCR using primers MR67 and MR145 (see

XX CC

XX AAW01601). The fusion protein has been produced in Sf9 Spodoptera

XX CC

XX frugiperda insect cells using a baculovirus expression system.

XX CC

XX The invention relates to molecules such as diabodies, trivalent and

XX CC

XX tetraivalent antibodies and small antigen binding peptides which can

XX CC

XX cross-link, or cross-react with, B7.1 and B7.2 expressed on

XX CC

XX professional antigen presenting cells leading to the inhibition of

XX CC

XX antigen-specific T cell activation. Methods to produce such

XX CC

XX molecules are provided. The molecules are used to treat or prevent

XX CC

XX diseases of the immune system, in particular graft rejection, graft

XX CC

XX versus host disease, allergy and autoimmune diseases (claimed).

XX XX

XX Sequence 251 AA;

XX SQ

XX Query Match

XX Best Local Similarity 99.5%; Pred. No. 5.1e-103;

XX Matches 215; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX QY

XX 1 GLSHFCSGVTHVTKVEKAVATLSGHNVSVEELAQTRIVYQKEKKVLTMTSGDMNIWPE 60

XX Db

XX 27 GLSHFCSGVTHVTKVEKAVATLSGHNVSVEELAQTRIVYQKEKKVLTMTSGDMNIWPE 86

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:23:30 ; Search time 14 Seconds
(without alignments)
453.954 Million cell updates/sec

Title: US-09-454-651B-23
Sequence: 1 GLSHFCGVIHVYKEVEA.....LRVNTFWNTTKQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	2	US-08-147-772-2
2	1149	100.0	288	2	US-08-456-104-6
3	1149	100.0	288	2	US-08-101-624-23
4	1149	100.0	288	2	US-08-751-767A-6
5	1149	100.0	288	3	US-08-153-262-2
6	1149	100.0	288	3	US-08-479-744A-29
7	1149	100.0	288	4	US-08-280-757B-29
8	1149	100.0	288	4	US-09-159-135-2
9	1149	100.0	288	4	US-08-205-697A-19
10	1149	100.0	288	4	US-08-702-525-19
11	1149	100.0	288	4	US-09-450-798-2
12	1149	100.0	288	4	US-08-403-253A-2
13	1149	100.0	288	4	US-09-651-200-13
14	1149	100.0	288	5	PCT-US95-02576-19
15	1149	100.0	473	4	US-09-171-945-131
16	1102	95.9	208	4	US-09-460-384-36
17	1100	95.7	288	4	US-09-651-200-14
18	1050	91.4	208	3	US-08-630-172-15
19	1050	91.4	208	4	US-09-375-419-15
20	743	64.7	292	4	US-09-651-200-16
21	738	64.2	299	4	US-09-651-200-15
22	561	48.8	306	4	US-08-205-697A-17
23	561	48.8	306	4	US-08-702-525-17
24	561	48.8	306	4	US-09-651-200-17
25	561	48.8	306	5	PCT-US95-02576-17
26	561	48.8	320	4	US-08-205-697A-2
27	561	48.8	320	4	US-08-702-525-2

Sequence 2, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 25, Appli
Sequence 4, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 63, Appli
Sequence 65, Appli

28 561 48.8 320 5 PCT-US95-02576-2
29 558 48.6 306 2 US-08-147-772-4
30 558 48.6 306 2 US-08-456-104-8
31 558 48.6 306 2 US-08-101-624-25
32 558 48.6 306 3 US-08-153-262-4
33 558 48.6 306 3 US-08-479-744A-31
34 558 48.6 306 4 US-08-280-757B-31
35 558 48.6 306 4 US-09-159-135-4
36 558 48.6 306 4 US-09-450-798-4
37 311 27.1 200 4 US-08-205-697A-9
38 311 27.1 200 4 US-08-702-525-9
39 311 27.1 200 5 PCT-US95-02576-9
40 311 27.1 214 4 US-08-205-697A-11
41 311 27.1 214 4 US-08-702-525-11
42 311 27.1 214 5 PCT-US95-02576-11
43 250.5 21.8 212 4 US-08-702-525-63
44 250.5 21.8 212 5 PCT-US95-02576-63
45 250.5 21.8 226 4 US-08-702-525-65

ALIGNMENTS

RESULT 1
US-08-147-772-2
; Sequence 2, Application US/08147772
; Patent No. 5858776
; GENERAL INFORMATION:
; APPLICANT: Ostrand-Rosenberg, Suzanne
; APPLICANT: Baskar, Sivasubramanian
; APPLICANT: Glimcher, Laurie H.
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M. Cells With Increased Immunogenicity
; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,772
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-147-772-2
Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVKVATLSCGHNVSVEELAQTRIYQKEKKMVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVKVATLSCGHNVSVEELAQTRIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADPPTS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSKLDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSKLDF 206
QY 181 NMTNHSFMCCLKYGLHVRVNTQFNNTTKQEHFPDN 216
DB 207 NMTNHSFMCCLKYGLHVRVNTQFNNTTKQEHFPDN 242
RESULT 2
US-08-456-104-6
Sequence 6, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456.104
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624;
FILING DATE: 26-JUL-1993;
APPLICATION NUMBER: 08/109,393;
APPLICATION NUMBER: 19-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids

```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-456-104-6

Query Match 100.0%; Score 1149; DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 60
   |||||||
Db 27 GLSHFCSGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKMWLTMSGDMNIWPE 86
   |||||||
QY 61 YKNRIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTPS 120
   |||||||
Db 87 YKNRIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTPS 146
   |||||||
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 180
   |||||||
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 206
   |||||||
QY 181 NMTNHSFCLIKYGLHRLVNOTFNWNTTKQEHFPDN 216
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Db 207 NMTNHSFCLIKYGLHRLVNOTFNWNTTKQEHFPDN 242

RESULT 3
US-08-101-624-23
; Sequence 23, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. 5942607el CTLA4/CD28 Ligands and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/101,624
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of
; IDENTIFICATION METHOD: soluble protein
; OTHER INFORMATION: hydrophobic
; FEATURE:
; NAME/KEY: extracellular domain
; LOCATION: 1 to 208
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 209 to 235
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: intracellular domain
; LOCATION: 236 to 254
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 19 to 21
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 55 to 57
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 64 to 66
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 152 to 154
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 173 to 175
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 177 to 179
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 192 to 194
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 198 to 200
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig V-set domain
; LOCATION: 1 to 104
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig C-set domain
; LOCATION: 105 to 202
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; PUBLICATION INFORMATION:
; AUTHORS: FREEMAN, GORDON J.
; AUTHORS: FREEDMAN, ARNOLD S.
; AUTHORS: SEGIL, JEFFREY M.
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IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: the Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-153-262-2
Query Match 100.0%; Score 1149; DB 3; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVKVATLSCHGNVSVEELAQTRIYVQKEKKMVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVKVATLSCHGNVSVEELAQTRIYVQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVSKADEPTPS 120
DB 87 YKNRTIFDITNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVSKADEPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSDPETELXAVSSKLD 180
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSDPETELXAVSSKLD 206
QY 181 NMTNHSFMCLIKYHLRVNQTFFNNTTKQEHFPDN 216
DB 207 NMTNHSFMCLIKYHLRVNQTFFNNTTKQEHFPDN 242
RESULT 6
US-08-479-744A-29
Sequence 29, Application US/08479744A
Patent No. 6084067
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6084067el CTLA4/CD28 Ligands and
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,744A
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/280,757
FILING DATE: 26-JUL-1994
APPLICATION NUMBER: 08/109,393
FILING DATE: 28-AUG-1993
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP3
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
NAME/KEY: Ig V-set domain

LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-479-744A-29
Query Match 100.0%; Score 1149; DB 3: Length 288;
Best Local Similarity 100.0%; Pred. No. 5,5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKWLTMTSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKWLTMTSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTYECVVKYKDAFKREHLAEVTLVKADFPPTPS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTYECVVKYKDAFKREHLAEVTLVKADFPPTPS 146
QY 121 ISDFEIPSTNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 180
DB 147 ISDFEIPSTNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDF 206
QY 181 NMTTNHSEFMCLIKYGLHVRVNTQFNNTTKQEHFPDN 216
DB 207 NMTTNHSEFMCLIKYGLHVRVNTQFNNTTKQEHFPDN 242
RESULT 7
US-08-280-757B-29
Sequence 29, Application us/08280757B
Patent No. 6130316
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
APPLICANT: Gray, Gary S.
APPLICANT: Greenfield, Edward
TITLE OF INVENTION: No. 6130316el CTLA4/CD28 Ligands and
TITLE OF INVENTION: Uses Therefor
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,757B
FILING DATE: 26-JUL-1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/101,624
FILING DATE: 26-JULY-1993
APPLICATION NUMBER: 08/109,393
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: 08/147,773
FILING DATE: 3-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-004CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262
US-08-280-757B-29
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYQKEKKVLTWMSGDMNIWPE 60
|||||
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYQKEKKVLTWMSGDMNIWPE 86
QY 61 YKNRTIFDTNNLSIVILALRPSDEGTTCVWLKYEKDAFKREHLAEVTLVKADFPPTS 120
|||||
Db 87 YKNRTIFDTNNLSIVILALRPSDEGTTCVWLKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
|||||
Db 147 ISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCILIKYGHRLRVNQTFNNTTKOEHPDN 216
|||||
Db 207 NMTNHSFMCILIKYGHRLRVNQTFNNTTKOEHPDN 242
RESULT 8
US-09-159-135-2
Sequence 2, Application US/09159135
Patent No. 6149905
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,135
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/147,772
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: 34 to 51
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence

FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEDMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-09-159-135-2
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVKEVATLSGHNVSVEELAQTRIVQKEKKMVLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVKEVATLSGHNVSVEELAQTRIVQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNNLSIVILALRPSDEGTGYECVVLKYKEDAFKREHLAEVTLVSKADPTPS 120
DB 87 YKNTIFDITNNLSIVILALRPSDEGTGYECVVLKYKEDAFKREHLAEVTLVSKADPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLPD 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLPD 206
QY 181 NMNTNHSFMCILIKYGLRVNQTFFNNNTTKQEHFPDN 216
DB 207 NMNTNHSFMCILIKYGLRVNQTFFNNNTTKQEHFPDN 242
RESULT 9
US-08-205-697A-19
; Sequence 19, Application US/08205697A
; Patent No. 621510
; GENERAL INFORMATION:

APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaolo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-205-697A-19
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDTNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDTNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLHRLVNTFNWNTTKQEHPPDN 216
Db 207 NMTNHSFMCILIKYGLHRLVNTFNWNTTKQEHPPDN 242
RESULT 10
US-08-702-525-19
Sequence 19, Application US/08702525
Patent No. 6294660
GENERAL INFORMATION:
APPLICANT: Sharpe, Sharpe
APPLICANT: Borriello, Francescopaolo
APPLICANT: Freeman, Gordon
APPLICANT: Nadler, Lee
TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
Molecules and Uses Therefor
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,525
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/205,697
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120CPUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-525-19
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNRTIFDTNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDTNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLHRLVNTFNWNTTKQEHPPDN 216
Db 207 NMTNHSFMCILIKYGLHRLVNTFNWNTTKQEHPPDN 242
RESULT 11
US-09-450-798-2
Sequence 2, Application US/09450798
Patent No. 6319709
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
APPLICANT: Baskar, Sivasubramanian
APPLICANT: Glimcher, Laurie H.
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/450,798
FILING DATE: 29-NOV-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/147,772
FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-09-450-798-2
Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVHVTKVEKAVTLSCGHNVSVLELAOTRIYWKQEKKMWLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVHVTKVEKAVTLSCGHNVSVLELAOTRIYWKQEKKMWLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYKEKDAFKREHLAEVTLVKADPPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNINTTVSQDPETELXAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNINTTVSQDPETELXAVSSKLD 206
QY 181 NMTTNHSMCLIKYCHLRVNTQTFNNTTKQEHFPDN 216
Db 207 NMTTNHSMCLIKYCHLRVNTQTFNNTTKQEHFPDN 242
RESULT 12
US-08-403-253A-2
Sequence 2, Application US/08403253A
Patent No. 6352694
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennett, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-cell
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts

COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/403,253A
 FILING DATE: March 10, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/253,964
 FILING DATE: 3 JUNE 1994
 APPLICATION NUMBER: US 08/073,223
 FILING DATE: 4 JUNE 1993
 APPLICATION NUMBER: US 08/200,947
 FILING DATE: 23 FEB 1994
 APPLICATION NUMBER: US 07/864,805
 FILING DATE: 7 APR 1992
 APPLICATION NUMBER: US 08/247,505
 FILING DATE: 23 MAY 1994
 APPLICATION NUMBER: US 07/864,866
 FILING DATE: 7 APR 1992
 APPLICATION NUMBER: US 08/218,155
 FILING DATE: 25 MAR 1994
 APPLICATION NUMBER: US 07/864,807
 FILING DATE: 7 APR 1992
 APPLICATION NUMBER: US 07/902,467
 FILING DATE: 16 JUNE 1992
 APPLICATION NUMBER: US 07/275,433
 FILING DATE: 23 NOV 1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragours, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: RPI-002CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 742-4214
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 DESCRIPTION: B cell activation antigen; natural ligand
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
 FEATURE:
 NAME/KEY: signal sequence
 LOCATION: -34 to -1
 IDENTIFICATION METHOD: amino terminal sequencing of
 IDENTIFICATION METHOD: soluble protein
 OTHER INFORMATION: hydrophobic
 FEATURE:
 NAME/KEY: extracellular domain
 LOCATION: 1 to 208
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: transmembrane domain
 LOCATION: 209 to 235
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: intracellular domain
 LOCATION: 236 to 254
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 19 to 21
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence

FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 55 to 57
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 64 to 66
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 152 to 154
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 173 to 175
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 177 to 179
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 192 to 194
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: N-linked glycosylation
 LOCATION: 198 to 200
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: Ig V-set domain
 LOCATION: 1 to 104
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 FEATURE:
 NAME/KEY: Ig C-set domain
 LOCATION: 105 to 202
 IDENTIFICATION METHOD: similarity with known
 IDENTIFICATION METHOD: sequence
 PUBLICATION INFORMATION:
 AUTHORS: FREEMAN, GORDON J.
 AUTHORS: FREEDMAN, ARNOLD S.
 AUTHORS: SEGIL, JEFFREY M.
 AUTHORS: LEE, GRACE
 AUTHORS: WHITMAN, JAMES F.
 AUTHORS: NADLER, LEE M.
 TITLE: B7, A New Member Of The Ig Superfamily With
 TITLE: Unique Expression On Activated And Neoplastic B Cells
 JOURNAL: The Journal of Immunology
 VOLUME: 143
 ISSUE: 8
 PAGES: 2714-2722
 DATE: 15-OCT-1989
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
 US-08-403-253A-2
 Query Match 100.0%; Score 1149; DB 4; Length 288;
 Best Local Similarity 100.0%; Pred No. 5,5e-113;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKKEKMYLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKKEKMYLTWMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTTCVWLYKYEKDAFKREHLAEVTLVSKADFTPS 120
 Db 87 YKNRTIFDITNNLSIVILALRPSDEGTTCVWLYKYEKDAFKREHLAEVTLVSKADFTPS 146

QY 121 ISDFEIPSTNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPSTNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCCLKYKGLRVNQTFFNNNTTKQEHFPD 216
Db 207 NMTNHSFMCCLKYKGLRVNQTFFNNNTTKQEHFPD 242

RESULT 13

US-09-651-200-13
; Sequence 13, Application US/09651200
; Patent No. 6429303
; GENERAL INFORMATION:
; APPLICANT: Green et al
; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B
; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 15966-562 (CURA-62)
; CURRENT APPLICATION NUMBER: US/09/651.200
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/152383
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/172909
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/183578
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-651-200-13

Query Match 100.0%; Score 1149; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKVEKVAITLSCGHNVSVEELAQTRIVQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKVEKVAITLSCGHNVSVEELAQTRIVQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPSTNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPSTNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCCLKYKGLRVNQTFFNNNTTKQEHFPD 216
Db 207 NMTNHSFMCCLKYKGLRVNQTFFNNNTTKQEHFPD 242

RESULT 14

PCT-US95-02576-19
; Sequence 19, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; TITLE OF INVENTION: and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-02576-19

Query Match 100.0%; Score 1149; DB 5; Length 288;
Best Local Similarity 100.0%; Pred. No. 5.5e-113;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKVEKVAITLSCGHNVSVEELAQTRIVQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKVEKVAITLSCGHNVSVEELAQTRIVQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPSTNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPSTNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCCLKYKGLRVNQTFFNNNTTKQEHFPD 216
Db 207 NMTNHSFMCCLKYKGLRVNQTFFNNNTTKQEHFPD 242

RESULT 15

US-09-171-945-131
; Sequence 131, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 131
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized

US-09-171-945-131

Query Match 100.0%; Score 1149; DB 4; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.2e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	27	GLSHFCSGVIHVTKEVKVATLSGCHNVSVBELAQTRIYWQEKKKMVLTMMSGDMNIWPE	86
Qy	61	YKNRTIFDITNNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVKADFPPTS	120
Db	87	YKNRTIFDITNNLSIVILALRPSDEGTGECVVLKYEKDAFKREHLAEVTLVKADFPPTS	146
Qy	121	ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD	180
Db	147	ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD	206
Qy	181	NMTTNHSPMCLIKYGHRLRVNOTFNWNTTKQEHFPDN	216
Db	207	NMTTNHSPMCLIKYGHRLRVNOTFNWNTTKQEHFPDN	242

Search completed: January 6, 2003, 14:25:51
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:25:11 ; Search time 11 Seconds
(without alignments)
372.139 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCGVIHVTKEVKEVA.....LRVNTQFNWNTTKQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	226	8	US-09-915-789A-21
2	1149	100.0	288	9	US-08-592-711-2
3	1149	100.0	288	9	US-09-896-738-10
4	1149	100.0	288	9	US-09-915-789A-15
5	1149	100.0	288	10	US-09-772-102-14
6	1149	100.0	288	10	US-09-837-867A-19
7	1149	100.0	288	10	US-09-910-174A-5
8	1149	100.0	473	10	US-09-910-059-131
9	1143	99.5	492	10	US-09-845-899A-3
10	1042	90.7	224	10	US-09-955-866-4
11	915	79.6	313	10	US-09-756-983-15
12	743	64.7	292	10	US-09-303-510-2
13	743	64.7	292	10	US-09-303-040-2
14	739	64.3	292	10	US-09-303-510-4
15	739	64.3	292	10	US-09-303-040-4
16	561	48.8	306	10	US-09-837-867A-17
17	561	48.8	320	10	US-09-837-867A-2
18	311	27.1	200	10	US-09-837-867A-9
19	311	27.1	214	10	US-09-837-867A-11

20	200.5	17.4	329	10	US-09-303-510-6	Sequence 6, Appli
21	200.5	17.4	329	10	US-09-303-040-6	Sequence 6, Appli
22	182	15.8	219	9	US-09-915-789A-22	Sequence 22, Appli
23	182	15.8	260	10	US-09-845-899A-5	Sequence 5, Appli
24	182	15.8	323	9	US-09-896-738-11	Sequence 11, Appli
25	182	15.8	323	9	US-09-915-789A-16	Sequence 16, Appli
26	182	15.8	323	10	US-09-955-866-5	Sequence 5, Appli
27	182	15.8	324	10	US-09-910-174A-6	Sequence 6, Appli
28	182	15.8	329	8	US-08-592-711-4	Sequence 4, Appli
29	182	15.8	329	10	US-09-837-867A-23	Sequence 23, Appli
30	182	15.8	351	10	US-09-756-983-18	Sequence 18, Appli
31	161	14.0	302	9	US-09-896-738-13	Sequence 13, Appli
32	161	14.0	302	10	US-09-789-561-136	Sequence 136, App
33	161	14.0	302	10	US-09-955-866-7	Sequence 7, Appli
34	161	14.0	309	10	US-09-910-174A-7	Sequence 7, Appli
35	161	14.0	344	10	US-09-764-853-812	Sequence 812, App
36	160	13.9	241	9	US-09-915-789A-11	Sequence 11, Appli
37	160	13.9	302	9	US-09-915-789A-18	Sequence 18, Appli
38	160	13.9	343	10	US-09-764-853-630	Sequence 630, App
39	160	13.9	345	10	US-09-764-853-810	Sequence 810, App
40	158.5	13.8	480	10	US-09-875-338-5	Sequence 5, Appli
41	156.5	13.6	220	9	US-09-915-789A-23	Sequence 23, Appli
42	156.5	13.6	245	9	US-10-068-215-2	Sequence 2, Appli
43	156.5	13.6	245	12	US-10-002-775-2	Sequence 2, Appli
44	156.5	13.6	290	9	US-10-068-215-4	Sequence 4, Appli
45	156.5	13.6	290	9	US-09-896-913A-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-915-789A-21
; Sequence 21, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match 100.0%; Score 1149; DB 9; Length 226;
Best Local Similarity 100.0%; Pred. No. 3.4e-86;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWKQKKMVLTMNSGDMNLTWE 60
Db 11 GLSHFCGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIYWKQKKMVLTMNSGDMNLTWE 70
QY 61 YKNRTIFDITNLSIVILALRPSDEGTCECVLKYKDKAFKREHLAEVTLTSVKADFPPTS 120
Db 71 YKNRTIFDITNLSIVILALRPSDEGTCECVLKYKDKAFKREHLAEVTLTSVKADFPPTS 130
QY 121 ISDFEPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINVTVSQDPETELYAVSSKLD 180
Db 131 ISDFEPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINVTVSQDPETELYAVSSKLD 190
QY 181 NMWTNSFCLIKYGLHRVNTQFNWNTTKQEHFPDN 216
Db 191 NMWTNSFCLIKYGLHRVNTQFNWNTTKQEHFPDN 226

RESULT 2
US-08-592-711-2
; Sequence 2, Application US/08592711
; Patent No. US20020115214A1
; GENERAL INFORMATION:
; APPLICANT: June, Carl H.
; APPLICANT: Thompson, Craig B.
; APPLICANT: Nabel, Gary J.
; APPLICANT: Gray, Gary S.
; APPLICANT: Rennett, Paul D.
; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,711
; FILING DATE: 26-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,816
; FILING DATE: 4-MAY-1995
; APPLICATION NUMBER: US 08/403,253
; FILING DATE: 10-MARCH-1995
; APPLICATION NUMBER: US 08/253,964
; FILING DATE: 3-JUNE-1994
; APPLICATION NUMBER: US 08/073,223
; FILING DATE: 4-JUNE-1993
; APPLICATION NUMBER: US 08/200,947
; FILING DATE: 23-FEB-1994
; APPLICATION NUMBER: US 07/864,805
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/247,505
; FILING DATE: 23-MAY-1994
; APPLICATION NUMBER: US 07/864,866
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 08/218,155
; FILING DATE: 25-MAR-1994
; APPLICATION NUMBER: US 07/864,807
; FILING DATE: 7-APR-1992
; APPLICATION NUMBER: US 07/902,467
; FILING DATE: 16-JUNE-1992
; APPLICATION NUMBER: US 07/275,433
; FILING DATE: 23-NOV-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-002CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: B cell activation antigen; natural ligand
; FEATURE:
; NAME/KEY: signal sequence
; LOCATION: -34 to -1
; IDENTIFICATION METHOD: amino terminal sequencing of
; IDENTIFICATION METHOD: soluble protein
; OTHER INFORMATION: hydrophobic

; FEATURE:
; NAME/KEY: extracellular domain
; LOCATION: 1 to 208
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 209 to 235
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: intracellular domain
; LOCATION: 236 to 254
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 19 to 21
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 55 to 57
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 64 to 66
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 152 to 154
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 173 to 175
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 177 to 179
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 192 to 194
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: N-linked glycosylation
; LOCATION: 198 to 200
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig V-set domain
; LOCATION: 1 to 104
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; FEATURE:
; NAME/KEY: Ig C-set domain
; LOCATION: 105 to 202
; IDENTIFICATION METHOD: similarity with known
; IDENTIFICATION METHOD: sequence
; PUBLICATION INFORMATION:
; AUTHORS: FREEMAN, GORDON J.
; AUTHORS: FREEDMAN, ARNOLD S.
; AUTHORS: SEGIL, JEFFREY M.
; AUTHORS: LEE, GRACE
; AUTHORS: WHITMAN, JAMES F.
; AUTHORS: NADLER, LEE M.
; TITLE: B7, A New Member Of The Ig Superfamily With

; TITLE: Unique Expression On Activated And Neoplastic B Cells
 ; JOURNAL: The Journal of Immunology
 ; VOLUME: 143
 ; ISSUE: 8
 ; PAGES: 2714-2722
 ; DATE: 15-OCT-1989
 ; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
 US-08-592-711-2

Query Match 100.0%; Score 1149; DB 8; Length 288;
 Best Local Similarity 100.0%; Pred. No. 4.5e-86;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 206
 QY 181 NMTTHSFMCILIKYGLHVRVNTFNNTTQOEHPDN 216
 DB 207 NMTTHSFMCILIKYGLHVRVNTFNNTTQOEHPDN 242

RESULT 3
 US-09-896-738-10
 ; Sequence 10, Application US/09896738
 ; Patent No. US20020165347A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fox, Michael
 ; APPLICANT: Sullivan, John K.
 ; APPLICANT: Fang, Mei
 ; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
 ; FILE REFERENCE: 00-513-A
 ; CURRENT FILING DATE: 2001-06-29
 ; PRIOR FILING DATE: 2001-06-29
 ; PRIOR FILING DATE: 2000-06-30
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 288
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-896-738-10

Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 4.5e-86;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 206
 QY 181 NMTTHSFMCILIKYGLHVRVNTFNNTTQOEHPDN 216
 DB 207 NMTTHSFMCILIKYGLHVRVNTFNNTTQOEHPDN 242

RESULT 4
 US-09-915-789A-15
 ; Sequence 15, Application US/09915789A
 ; Patent No. US20020168762A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Lieping
 ; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
 ; MOLECULES
 ; FILE REFERENCE: 07039-219001
 ; CURRENT APPLICATION NUMBER: US/09/915,789A
 ; CURRENT FILING DATE: 2002-06-04
 ; PRIOR APPLICATION NUMBER: US 60/220,991
 ; PRIOR FILING DATE: 2000-07-27
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 288
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-915-789A-15

Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 4.5e-86;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 60
 DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPE 86
 QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
 DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVCVVLKYEKDAFKREHLAEVTLVKADFPPTS 146
 QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 206
 QY 181 NMTTHSFMCILIKYGLHVRVNTFNNTTQOEHPDN 216
 DB 207 NMTTHSFMCILIKYGLHVRVNTFNNTTQOEHPDN 242

RESULT 5
 US-09-772-102-14
 ; Sequence 14, Application US/09772102
 ; Patent No. US2002006413A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sobol, Robert, E.
 ; APPLICANT: Shawler, Daniel L.
 ; APPLICANT: Bartholomew, Richard M.
 ; APPLICANT: Carlo, Dennis J.
 ; APPLICANT: Gold, Daniel P.
 ; TITLE OF INVENTION: Genetically Engineered Tumor Cell
 ; FILE REFERENCE: P-SD 4581
 ; CURRENT APPLICATION NUMBER: US/09/772,102
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: US 60/178,498
 ; PRIOR FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/185,335
 ; PRIOR FILING DATE: 2000-02-28
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 288
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-772-102-14

Query Match 100.0%; Score 1149; DB 10; Length 288;
 Best Local Similarity 100.0%; Pred. No. 4.5e-86;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLSHFCSGVTHVTKEVKEVATLSGHNHVSVEELAQTRIYQWEKKMVLTMWSGDMNIWPE	60
Db	27	GLSHFCSGVTHVTKEVKEVATLSGHNHVSVEELAQTRIYQWEKKMVLTMWSGDMNIWPE	86
QY	61	YKNRTIFDITNNLSIVILARPSDEGTYECVWLKYEKDAFKREHLAEVTLVSKADPPTPS	120
Db	87	YKNRTIFDITNNLSIVILARPSDEGTYECVWLKYEKDAFKREHLAEVTLVSKADPPTPS	146
QY	121	ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSQDPETELVAVSSKLPD	180
Db	147	ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTVSQDPETELVAVSSKLPD	206
QY	181	NMTNHSFMCILIKYGLHRVNOTFNWNTTKOEHPDN	216
Db	207	NMTNHSFMCILIKYGLHRVNOTFNWNTTKOEHPDN	242

RESULT 6

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US-09-837-867A-19
; Sequence 19, Application US/09837867A
; Patent No. US20020098542A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Arlene H.
; APPLICANT: Borriello, Francescopaulo
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: No. US20020098542A1el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; FILE REFERENCE: BWI-120CPADV
; CURRENT APPLICATION NUMBER: US/09/837,867A
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 08/205,697
; PRIOR FILING DATE: 1994-03-02
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-837-867A-19

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RESULT 7

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US-09-910-174A-5
RESOLUTION /
; Sequence 5, Application US/09910174A
; Patent No. US20020106730A1
; GENERAL INFORMATION:
; APPLICANT: Coyle, Anthony J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Manning, Stephen
; TITLE OF INVENTION: B7-H2 Molecules, No. US20020106730A1
; TITLE OF INVENTION: Family and Uses Thereof
; FILE REFERENCE: 35800/236924
Members of the B7

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; CURRENT APPLICATION NUMBER: US/09/910,174A
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 09/620,461
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 288
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-910-174A-5

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RESULT 8

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US-09-910-059-131
; Sequence 131, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion
US-09-910-059-131

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Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 206
Qy 181 NMTNHSFMCILKYGHLRVNQTFFNNTTKQEHFPD 216
Db 207 NMTNHSFMCILKYGHLRVNQTFFNNTTKQEHFPD 242

RESULT 9

US-09-845-899A-3
; Sequence 3, Application US/09845899A
; Patent No. US20020147326A1
; GENERAL INFORMATION:
; APPLICANT: CHAIKIN, MARGERY ANN
; APPLICANT: LYNN, SALLY DOREEN PATRICIA
; APPLICANT: SWEET, RAYMOND W.
; APPLICANT: TRUNEH, ALEMSEGED
; TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES
; FILE REFERENCE: P50496
; CURRENT APPLICATION NUMBER: US/09/845,899A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/202,346
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/043,948
; PRIOR FILING DATE: 1997-02-19
; PRIOR APPLICATION NUMBER: US 60/038,915
; PRIOR FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 492
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-845-899A-3

Query Match 99.5%; Score 1143; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 2.6e-85;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWKKEKMWLTMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWKKEKMWLTMSGDMNIWPE 86
Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 206
Qy 181 NMTNHSFMCILKYGHLRVNQTFFNNTTKQEHFPD 215
Db 207 NMTNHSFMCILKYGHLRVNQTFFNNTTKQEHFPD 241

RESULT 10

US-09-955-866-4
; Sequence 4, Application US/09955866
; Patent No. US20020107363A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Holst, Paige
; APPLICANT: Yoshinaga, Steven Kiyoshi
; TITLE OF INVENTION: B7-Like Polypeptides and Uses Thereof
; FILE REFERENCE: 00,759-A
; CURRENT APPLICATION NUMBER: US/09/955,866

; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,867
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-955-866-4

Query Match 90.7%; Score 1042; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e-77;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWKKEKMWLTMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWKKEKMWLTMSGDMNIWPE 86
Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 206
Qy 181 NMTNHSFMCILKYGHLR 198
Db 207 NMTNHSFMCILKYGHLR 224

RESULT 11

US-09-756-983-15
; Sequence 15, Application US/09756983
; Patent No. US20020122818A1
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion constructs with human and bacterial sequences
US-09-756-983-15

Query Match 79.6%; Score 915; DB 10; Length 313;
Best Local Similarity 100.0%; Pred. No. 4.3e-67;
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWKKEKMWLTMSGDMNIWPE 60
Db 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWKKEKMWLTMSGDMNIWPE 86
Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVS 175

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Db 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVS 201
|||||
RESULT 12
US-09-303-510-2
; Sequence 2, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisison, Ellen W.
; APPLICANT: Hash, Stephen M.
; APPLICANT: Choi, InSoo
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides
; FILE REFERENCE: 54954
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-2

Query Match 64.7%; Score 743; DB 10; Length 292;
Best Local Similarity 63.3%; Pred. No. 3.3e-53;
Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVIHVTKEYEVATLSGHNVSVEELAQTIRYQKEKKMVLTMMSGDMNIWPEY 61
Db 28 LFYFCGGIIQVKNKTVEEAVLSCDYNISTKELTEIRIYQKDDVMVAVMSGKVQWPKY 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTSI 121
Db 88 KNRTFTVDNHSIVIMALRSLDSNGKYTCIIQKIEGSKYKHLTSVMLLVRAFPVPSI 147
QY 122 SDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSKLDFN 181
Db 148 TDLGNPSHNIRKIMCLTSGGPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDEN 207
QY 182 MTNHSFMCILKYGHLRVNQTENNNTTQEHFPDN 216
Db 208 MTNHSFCLVKYGNLLVSQIFNQ--KSEPQPSN 240

RESULT 14
US-09-303-510-4
; Sequence 4, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisison, Ellen W.
; APPLICANT: Hash, Stephen M.
; APPLICANT: Choi, InSoo
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides
; FILE REFERENCE: 54954
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-4

Query Match 64.3%; Score 739; DB 10; Length 292;
Best Local Similarity 62.8%; Pred. No. 7e-53;
Matches 135; Conservative 34; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVIHVTKEYEVATLSGHNVSVEELAQTIRYQKEKKMVLTMMSGDMNIWPEY 61
Db 28 LFYFCGGIIQVKNKTVEEAVLSCDYNISTKELTEIRIYQKDDVMVAVMSGKVQWPKY 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTSI 121
Db 88 KNRTFTVDNHSIVIMALRSLDSNGKYTCIIQKIEGSKYKHLTSVMLLVRAFPVPSI 147
QY 122 SDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSKLDFN 181
Db 148 TDLGNPSHNIRKIMCLTSGGPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDEN 207
QY 182 MTNHSFMCILKYGHLRVNQTENNNTTQEHFPDN 216
Db 208 MTNHSFCLVKYGNLLVSQIFNQ--KSEPQPSN 240

RESULT 15
US-09-303-040-4
; Sequence 4, Application US/09303040
; Patent No. US20020051792A1
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
; TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof
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Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVIHVTKEYEVATLSGHNVSVEELAQTIRYQKEKKMVLTMMSGDMNIWPEY 61
Db 28 LFYFCGGIIQVKNKTVEEAVLSCDYNISTKELTEIRIYQKDDVMVAVMSGKVQWPKY 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTSI 121
Db 88 KNRTFTVDNHSIVIMALRSLDSNGKYTCIIQKIEGSKYKHLTSVMLLVRAFPVPSI 147
QY 122 SDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSKLDFN 181
Db 148 TDLGNPSHNIRKIMCLTSGGPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDEN 207
QY 182 MTNHSFMCILKYGHLRVNQTENNNTTQEHFPDN 216
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RESULT 14
US-09-303-510-4
; Sequence 4, Application US/09303510A
; Patent No. US20020028208A1
; GENERAL INFORMATION:
; APPLICANT: Collisison, Ellen W.
; APPLICANT: Hash, Stephen M.
; APPLICANT: Choi, InSoo
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, and Feline
; TITLE OF INVENTION: CTLA-4 Nucleic Acid and Polypeptides
; FILE REFERENCE: 54954
; CURRENT APPLICATION NUMBER: US/09/303,510A
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,869
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Feline
US-09-303-510-4

Query Match 64.3%; Score 739; DB 10; Length 292;
Best Local Similarity 62.8%; Pred. No. 7e-53;
Matches 135; Conservative 34; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVIHVTKEYEVATLSGHNVSVEELAQTIRYQKEKKMVLTMMSGDMNIWPEY 61
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QY 62 KNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVSKADFPPTSI 121
Db 88 KNRTFTVDNHSIVIMALRSLDSNGKYTCIIQKIEGSKYKHLTSVMLLVRAFPVPSI 147
QY 122 SDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSKLDFN 181
Db 148 TDLGNPSHNIRKIMCLTSGGPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDEN 207
QY 182 MTNHSFMCILKYGHLRVNQTENNNTTQEHFPDN 216
Db 208 MTNHSFCLVKYGNLLVSQIFNQ--KSEPQPSN 240

RESULT 15
US-09-303-040-4
; Sequence 4, Application US/09303040
; Patent No. US20020051792A1
; GENERAL INFORMATION:
; APPLICANT: Winslow, Barbara J.
; APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: Recombinant Virus Expressing Foreign DNA Encoding
; TITLE OF INVENTION: Feline CD80, Feline CD86, Feline CD28, Feline CTLA-4 or
; TITLE OF INVENTION: Feline Interferon-gamma And Uses Thereof
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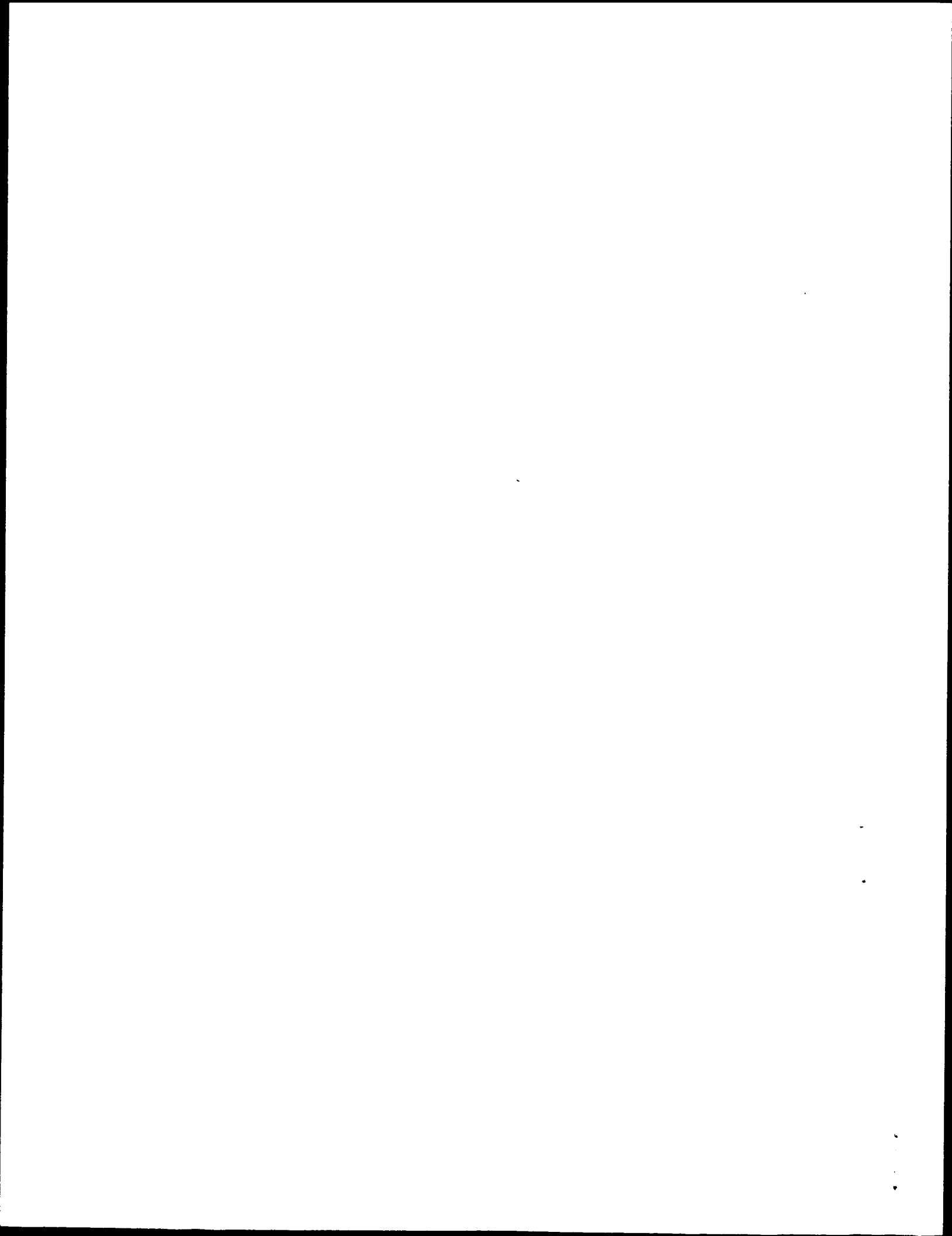


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; FILE REFERENCE: 54957-B
; CURRENT APPLICATION NUMBER: US/09/303,040
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 60/083,870
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 292
; TYPE: PRT
; ORGANISM: feline CD80
US-09-303-040-4
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Best Local Similarity 62.8%; Pred. No. 7e-53;
Matches 135; Conservative 34; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVIHVTKEVATLSCGHNVSEELAOPTRIYQKEKMKVLTMMSGDMNIWPEY 61
DB 28 LEYFCGIIQVKNKTVEEVAVLSCDYNISTKELTEIRIYQKDDENVLAVMSGKVQVWPY 87
QY 62 KNRTIFDTNNLSIVILALRPSDEGTYECVILKYEKDAFKREHLEAVTLISKADPTPSI 121
DB 88 KNRTFTDVTNHSIVIMALRLSDNGKTYTCIIQIKQGSYKVKHLTSVMLLVRADEFVPSI 147
QY 122 SDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 181
DB 148 TDGPNFSNIRKIMCLTSGGPPKPHLSWLENEEELNAINTTVSQDPETELYTISSELDNF 207
QY 182 MTNHSFMCILIKYHRLVNTQFNWNTTKOEHPDN 216
DB 208 MTNHSFCLVLYGNLIVSQIENWQ--KSEPOPSN 240
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Search completed: January 6, 2003, 14:29:02
Job time : 12 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2003, 14:24:10 ; Search time 143 Seconds

(without alignments)
973.863 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
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- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	216	8 US-08-459-766B-8	Sequence 8, Appli
2	1149	100.0	216	18 US-09-454-651B-23	Sequence 23, Appli
3	1149	100.0	216	19 US-09-569-164A-8	Sequence 8, Appli
4	1149	100.0	226	1 PCT-US01-41430-21	Sequence 21, Appli
5	1149	100.0	226	23 US-09-915-789A-21	Sequence 21, Appli
6	1149	100.0	248	1 PCT-US01-06769-12	Sequence 12, Appli

7	1149	100.0	288	1 PCT-US01-41430-15	Sequence 15, Appli
8	1149	100.0	288	1 PCT-US02-09671-1947	Sequence 1947, Ap
9	1149	100.0	288	1 PCT-US02-09671-1948	Sequence 1948, Ap
10	1149	100.0	288	1 PCT-US02-09671-1949	Sequence 1949, Ap
11	1149	100.0	288	1 PCT-US02-09671-1950	Sequence 1950, Ap
12	1149	100.0	288	1 PCT-US02-09671-1951	Sequence 1951, Ap
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15	1149	100.0	288	1 PCT-US02-09671-1956	Sequence 1956, Ap
16	1149	100.0	288	1 PCT-US02-09671-1958	Sequence 1958, Ap
17	1149	100.0	288	1 PCT-US02-09671-1961	Sequence 1961, Ap
18	1149	100.0	288	1 PCT-US02-09671-1962	Sequence 1962, Ap
19	1149	100.0	288	1 PCT-US02-09671-1966	Sequence 1966, Ap
20	1149	100.0	288	1 PCT-US02-09671-1967	Sequence 1967, Ap
21	1149	100.0	288	1 PCT-US02-09671-1968	Sequence 1968, Ap
22	1149	100.0	288	1 PCT-US02-09671-1969	Sequence 1969, Ap
23	1149	100.0	288	1 PCT-US02-09671-1970	Sequence 1970, Ap
24	1149	100.0	288	3 US-07-751-306C-2	Sequence 2, Appli
25	1149	100.0	288	5 US-08-109-393A-29	Sequence 29, Appli
26	1149	100.0	288	5 US-08-147-773-6	Sequence 6, Appli
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35	1149	100.0	288	17 US-09-349-915A-2	Sequence 2, Appli
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37	1149	100.0	288	17 US-09-350-202-2	Sequence 2, Appli
38	1149	100.0	288	17 US-09-368-581-6	Sequence 6, Appli
39	1149	100.0	288	18 US-09-425-516-29	Sequence 29, Appli
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41	1149	100.0	288	19 US-09-522-206-2	GENERAL INFORMA
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45	1149	100.0	288	20 US-09-620-461-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-459-766B-8
; Sequence 8, Application US/08459766B
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
; FILE REFERENCE: 30436.11US04
; CURRENT APPLICATION NUMBER: US/08/459,766B
; CURRENT FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/498,949
; PRIOR FILING DATE: 1990-03-26
; PRIOR APPLICATION NUMBER: 07/547,980
; PRIOR FILING DATE: 1990-07-02
; PRIOR APPLICATION NUMBER: 07/722,101
; PRIOR FILING DATE: 1991-06-27
; PRIOR APPLICATION NUMBER: 08/219,200
; PRIOR FILING DATE: 1994-03-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Freedman, Gordon J.
; AUTHORS: Freedman, Arnold S.

; AUTHORS: Segil, Jeffrey M.
; AUTHORS: Lee, Grace
; AUTHORS: Whitman, James F.
; AUTHORS: Nadler, Lee M.
; TITLE: B7, A NEW MEMBER OF THE Ig SUPERFAMILY WITH UNIQUE
; TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
; JOURNAL: J. Immunol.
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 1989-10-15
; RELEVANT RESIDUES: 1 TO 216
US-08-459-766B-8

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Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 YKNRTIFDTNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADFPPTS 120
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELVAVSSKLDF 180
DB 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELVAVSSKLDF 180
QY 181 NMTNHSFMCCLKYGHRLVNTQFNNTTKQEHFPDN 216
DB 181 NMTNHSFMCCLKYGHRLVNTQFNNTTKQEHFPDN 216

RESULT 2

US-09-454-651B-23
; Sequence 23, Application US/09454651B
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; Ledbetter, Jeffrey A.
; Damle, Nitin K.
; Brady, William
; Wallace, Philip M.
; TITLE OF INVENTION: CD14/CD38Ig HYBRID FUSION
; CORRESPONDENCE ADDRESS:
; ADDRESS: Mandel & Adriano
; STREET: 35 N. Arroyo Parkway, Suite 60
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/454,651B
; FILING DATE: 06-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/228,208
; FILING DATE: 15-APR-1994
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B
; REGISTRATION NUMBER: 34,470

; REFERENCE/DOCKET NUMBER: 30436.30USD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 626 395-7801
; TELEFAX: 626 395-0694
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 216 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-454-651B-23

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Best Local Similarity 100.0%; Pred. No. 8.3e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 NMTNHSFMCCLKYGHRLVNTQFNNTTKQEHFPDN 216
DB 181 NMTNHSFMCCLKYGHRLVNTQFNNTTKQEHFPDN 216

RESULT 3

US-09-569-164A-8
; Sequence 8, Application US/09569164A
; GENERAL INFORMATION:
; APPLICANT: LINSLEY, PETER S. ET AL.
; TITLE OF INVENTION: LIGAND FOR CD28 RECEPTOR ON B CELLS AND METHODS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/569,164A
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 07/547,980
; PRIOR FILING DATE: 1990-07-02
; PRIOR APPLICATION NUMBER: 07/722,101
; PRIOR FILING DATE: 1991-06-27
; PRIOR APPLICATION NUMBER: 08/219,200
; PRIOR FILING DATE: 1994-03-29
; PRIOR APPLICATION NUMBER: 08/459,766
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Freeman, Gordon J.
; AUTHORS: Freedman, Arnold S.
; AUTHORS: Segil, Jeffrey M.
; AUTHORS: Lee, Grace
; AUTHORS: Whitman, James F.
; AUTHORS: Nadler, Lee M.
; TITLE: B7, A NEW MEMBER OF THE Ig SUPERFAMILY WITH UNIQUE
; TITLE: EXPRESSION ON ACTIVATED AND NEOPLASTIC B CELLS
; JOURNAL: J. Immunol.
; VOLUME: 143
; ISSUE: 8
; PAGES: 2714-2722
; DATE: 1989-10-15

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; RELEVANT RESIDUES: 1 TO 216
US-09-569-164A-8

Query Match      100.0%; Score 1149; DB 19; Length 216;
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Db 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKEDAFKREHLAEVTLVKADFPPTS 120

QY 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180
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Db 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180

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Db 181 NMTNHSFMCCLKYGHRLRVNQTFFNNTTKQEHFPDN 216

RESULT 4
PCT-US01-41430-21
; Sequence 21, Application PC/TUS0141430
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219W01
; CURRENT APPLICATION NUMBER: PCT/US01/41430
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/220,991
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-41430-21

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RESULT 5
US-09-915-789A-21
; Sequence 21, Application US/09915789A
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219001
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; CURRENT APPLICATION NUMBER: US/09/915.789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match      100.0%; Score 1149; DB 23; Length 226;
Best Local Similarity 100.0%; Pred. No. 8.9e-112;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWKQKKMVLTMMSGDMNIWPE 70

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKEDAFKREHLAEVTLVKADFPPTS 120
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Db 71 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKEDAFKREHLAEVTLVKADFPPTS 130

QY 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180
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Db 131 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 190

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Db 191 NMTNHSFMCCLKYGHRLRVNQTFFNNTTKQEHFPDN 226

RESULT 6
PCT-US01-06769-12
; Sequence 12, Application PC/TUS0106769
; GENERAL INFORMATION:
; APPLICANT: Mayo Medical Ventures
; TITLE OF INVENTION: hb7-H2, A NOVEL CO-STIMULATORY MOLECULE
; FILE REFERENCE: 07039-202W01
; CURRENT APPLICATION NUMBER: PCT/US01/06769
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/186,519
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-06769-12

Query Match      100.0%; Score 1149; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 1e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWKQKKMVLTMMSGDMNIWPE 60
   |||||||
Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWKQKKMVLTMMSGDMNIWPE 86

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKEDAFKREHLAEVTLVKADFPPTS 120
   |||||||
Db 87 YKNRTIFDITNNLSIVILALRPSDEGTCECVLKYKEDAFKREHLAEVTLVKADFPPTS 146

QY 121 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180
   |||||||
Db 147 ISDFEIPTSNIRRIICSTSGGPPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 206

QY 181 NMTNHSFMCCLKYGHRLRVNQTFFNNTTKQEHFPDN 216
   |||||||
Db 207 NMTNHSFMCCLKYGHRLRVNQTFFNNTTKQEHFPDN 242
```

RESULT 7
PCT-US01-41430-15
; Sequence 15, Application PC/TUS0141430
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; MOLECULES
; FILE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219W01
; CURRENT APPLICATION NUMBER: PCT/US01/41430
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-41430-15

Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKAVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKAVLTMMSGDMNIWPE 86

QY 61 YKNRTIFDTNNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDTNNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 146

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYSKLDLF 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYSKLDLF 206

QY 181 NMTNHSFMCCLKYGLHVRNQTNNNTTQEHFPDN 216
Db 207 NMTNHSFMCCLKYGLHVRNQTNNNTTQEHFPDN 242

RESULT 8
PCT-US02-09671-1947
; Sequence 1947, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1947
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1947

Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKAVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKAVLTMMSGDMNIWPE 86

QY 61 YKNRTIFDTNNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDTNNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 146

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYSKLDLF 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYSKLDLF 206

QY 181 NMTNHSFMCCLKYGLHVRNQTNNNTTQEHFPDN 216
Db 207 NMTNHSFMCCLKYGLHVRNQTNNNTTQEHFPDN 242

RESULT 9
PCT-US02-09671-1948
; Sequence 1948, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1948
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1948

Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKAVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYWQEKKAVLTMMSGDMNIWPE 86

QY 61 YKNRTIFDTNNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNRTIFDTNNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVKADFPPTS 146

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYSKLDLF 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYSKLDLF 206

QY 181 NMTNHSFMCCLKYGLHVRNQTNNNTTQEHFPDN 216
Db 207 NMTNHSFMCCLKYGLHVRNQTNNNTTQEHFPDN 242

RESULT 10
PCT-US02-09671-1949
; Sequence 1949, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.

```
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1949
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1949
```

```
Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 60
|||||
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 86
|||||

QY 61 YKNTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
|||||
DB 87 YKNTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146
|||||

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 180
|||||
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 206
|||||

QY 181 NMTNHSFMCILIKYGHRLRVNQTFFNMNTTKQEHFPDN 216
|||||
DB 207 NMTNHSFMCILIKYGHRLRVNQTFFNMNTTKQEHFPDN 242
|||||
```

```
RESULT 11
PCT-US02-09671-1950
; Sequence 1950, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: ZYCOS Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1950
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1950
```

```
Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 60
|||||
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 86
|||||

QY 61 YKNTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
|||||
DB 87 YKNTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146
|||||

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 180
|||||
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 206
|||||

QY 181 NMTNHSFMCILIKYGHRLRVNQTFFNMNTTKQEHFPDN 216
|||||
DB 207 NMTNHSFMCILIKYGHRLRVNQTFFNMNTTKQEHFPDN 242
|||||
```

```
RESULT 12
PCT-US02-09671-1951
; Sequence 1951, Application PC/TUS0209671
; GENERAL INFORMATION:
; APPLICANT: ZYCOS Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: PCT/US02/09671
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1951
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-09671-1951
```

```
Query Match 100.0%; Score 1149; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 60
|||||
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVVEELAQTRIYWQEKKMWLTMMSGDMNIWPE 86
|||||

QY 61 YKNTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 120
|||||
DB 87 YKNTIFDITNNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLVKADFPPTS 146
|||||

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 180
|||||
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDLF 206
|||||

QY 181 NMTNHSFMCILIKYGHRLRVNQTFFNMNTTKQEHFPDN 216
|||||
DB 207 NMTNHSFMCILIKYGHRLRVNQTFFNMNTTKQEHFPDN 242
|||||
```

RESULT 13

us-09-454-651b-23.rapm

Tue Jan 7 09:21:48 2003

Db 207 NMTNHSFMCCLKYGHRLRVNQTFFNWTTKQEHFPDN 242

Search completed: January 6, 2003, 14:28:21
Job time : 145 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:23:10 ; Search time 21 seconds

(without alignments)
988.811 Million cell updates/sec

Title: US-09-454-651b-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVIHVTKEVKEVA.....LRVNTQFNNTTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	A45803	B-cell-restricted
2	1085	94.4	289	G00031	B7 protein - red-c
3	738	64.2	299	I46690	CD80 precursor - r
4	601.5	52.3	321	I54766	B-lymphocyte activ
5	561	48.8	309	I49503	B-lymphocyte activ
6	185	16.1	275	JC7604	CD86 spliced varia
7	182	15.8	329	I48754	B7-2 antigen - hum
8	152	13.2	309	I49522	gene B7-2 protein
9	140.5	12.2	330	I46691	CD86 precursor - r
10	133.5	11.6	583	I39428	alcam - human
11	129	11.2	221	Q0BE48	BARF1 protein - hu
12	127	11.1	526	S70587	butyrophilin precu
13	122.5	10.7	588	JH0506	adhesion molecule
14	122.5	10.7	588	A45254	surface glycoprote
15	120.5	10.5	509	JC5288	SHP substrate-1 pr
16	120.5	10.5	513	JC5289	SHP substrate-1 pr
17	118	10.3	487	S65133	butyrophilin - mou
18	116.5	10.1	1088	IJXLNL	neural cell adhesi
19	115	10.0	761	IJHUNG	neural cell adhesi
20	112.5	9.8	725	JE0099	DM-GRASP precursor
21	110.5	9.6	587	JH0464	cell surface glyco
22	109.5	9.5	646	I38049	neural cell adhesi
23	109.5	9.5	853	IJBONC	butyrophilin - bov
24	109	9.5	526	I37821	protein-tyrosine-p
25	109	9.5	2029	TDPELK	protein-tyrosine k
26	108	9.4	871	I48696	protein-tyrosine k
27	108	9.4	881	I48697	hypothetical prote
28	107.5	9.4	5175	T20992	hemocentin precurs
29	107.5	9.4	5198	T43290	

ALIGNMENTS

RESULT 1

A45803

B-cell-restricted antigen B7 precursor - human

N:Alternate names: B-lymphocyte activation antigen B7

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Sep-1999

C:Accession: I54495; A45803

R:Selvakumar, A.; Mohanraj, B.K.; Eddy, R.L.; Shows, T.B.; White, P.C.; Dupont, B.

Immunogenetics 36, 175-181, 1992

A:Title: Genomic organization and chromosomal location of the human gene encoding the

A:Reference number: I54495; MUID:92307753; PMID:1377173

A:Accession: I54495

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-288 <RES>

A:Cross-references: GB:M83077; NID:g179327; PIDN:AAA58990.1; PID:g179329

J:Freeman, G.J.; Freedman, A.S.; Segil, J.M.; Lee, G.; Whitman, J.F.; Nadler, L.M.

R:Immunol. 143, 2714-2722, 1989

A:Title: B7, a new member of the Ig superfamily with unique expression on activated a

A:Reference number: A45803; MUID:90010147; PMID:2794510

A:Accession: A45803

A:Molecule type: mRNA

A:Residues: 1-288 <FRE>

A:Cross-references: GB:M27533; NID:g184680; PIDN:AAA36045.1; PID:g306916

C:Genetics:

A:Gene: GDB:CD80; CD28LG1; CD28

A:Cross-references: GDB:251792; OMIM:112203

A:Map position: 3q13.3-3q21

A:Introns: 34/1; 140/1; 234/1; 266/1

C:Superfamily: B-lymphocyte restricted antigen B7

C:Keywords: transmembrane protein

F:1-26/Domain: signal sequence #status predicted <SIG>

F:248-264/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 1149; DB 2; Length 288;

Best Local Similarity 100.0%; Pred. No. 2e+85; Indels 0; Gaps 0;

Matches 216; Conservative 0; Mismatches 0;

QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIVYQKEKKMVLTMMSGDMNTWPE 60

Db 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVVEELAQTRIVYQKEKKMVLTMMSGDMNTWPE 86

QY 61 YKNTTFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLTSVKADFTPS 120

Db 87 YKNTTFDITNNLSIVILALRPSDEGTYECVWLKYEKDAFKREHLAEVTLTSVKADFTPS 146

QY 121 ISDFEPTSNIRRICSTSGGFPPEPHLSWLENGEELNAINTVSQDPETELIVYSSKLDLF 180

Db 147 ISDFEPTSNIRRICSTSGGFPPEPHLSWLENGEELNAINTVSQDPETELIVYSSKLDLF 206

QY 181 NMTNHSFMCILIKYGLRVNQTFNNTTKQEHFPDN 216

|||||

Db 207 NMTNHSFMCILIKYGHRLRVNQTNNWTTKQEHFPDN 242

RESULT 2
G00031
B7 protein - red-crowned mangabey (fragment)
C:Species: Cercopithecus torquatus (red-crowned mangabey, white-collared mangabey)
C:Date: 11-Apr-1997 #sequence_revision 11-Apr-1997 #text_change 29-Sep-1999
C:Accession: G00031
R:Villinger, F.J.
submitted to the EMBL Data Library, January 1995
A:Reference number: G00217
A:Accession: G00031
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-289 <VIL>
A:Cross-references: EMBL:U19833; NID:g644783; PIDN:AAA86700.1; PID:g644784
C:Genetics:
A:Gene: B7
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 94.4%; Score 1085; DB 2; Length 289;
Best Local Similarity 95.3%; Pred. No. 3e-80;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVHVTKEVKEVATLSCHGNVSVVEELAQTRIIYQKEKKMVLTMMSGDMNIWPEY 61
|||||
Db 28 LSHFCSGVHVTKEVKEVATLSCHGNVSVVEELAQTRIIYQKEKKMVLTMMSGDMNIWPEY 87
|||||

QY 62 KNTTIEDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVSKADFTPTPSI 121
|||||
Db 88 KNTTIEDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVSKADFTPTPSI 147
|||||

QY 122 SPEIPTSNIRRICTSGGFPPEHLSWLENGEELNAINTTVSQDPETELVAVSSKLDEN 181
|||||
Db 148 TDFEIPSPNIRRICTSGGFPPEHLSWLENGEELNAINTTVSQDPETELVAVSSKLDEN 207
|||||

QY 182 MTNHSFMCILIKYGHRLRVNQTNNWTTKQEHFPDN 216
|||||
Db 208 MTNHSFMCILIKYGHRLRVNQTNNWTTKQEHFPDN 242
|||||

RESULT 3
I46690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 29-Sep-1999
C:Accession: I46690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A:Reference number: I46689; MUID:95369849; PMID:7642234
A:Accession: I46690
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-299 <ISO>
A:Cross-references: GB:D49843; NID:g755096; PIDN:BAA08643.1; PID:g755097
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 64.2%; Score 738; DB 2; Length 299;
Best Local Similarity 63.9%; Pred. No. 3.2e-52;
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

QY 4 HFCSGVIHVTKEVATLSCHGNVSVVEELAQTRIIYQKEKKMVLTMMSGDMNIWPEYKN 63
|||||
Db 29 HFSGISQVTSVKREMAALSDYINISIDELAMRIYQKDDQMVLSIISGQVEVWPEYKN 88
|||||

QY 64 RTIFDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVSKADFTPTPSISD 123
|||||
Db 89 RTFDPDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVSKADFTPTPSISD 148
|||||

QY 124 FEIPTSNIIRRICTSGGFPPEHLSWLENGEELNAINTTVSQDPETELVAVSSKLDENMT 183
|||||

Db 149 IGHPDPNVKIRCSASGGFPPELAWMEDGELNAINTTVDQDLDTELYSVSSSELDFTNT 208

QY 184 TNHSFMCILIKYGHRLRVNQTNNWTTKOE 211
|||||

Db 209 NNHSIVCLIKYGELSVSQIFPWSKPQOE 236
|||||

RESULT 4
I54766
B-lymphocyte activation antigen 7-1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 19-May-2000
C:Accession: I54766
R:Judge, T.A.; Liu, M.; Christensen, P.J.; Pak, J.J.; Turka, L.A.
Int. Immunol. 7, 171-178, 1995
A:Title: Cloning the rat homolog of the CD28/CTLA-4-ligand B7-1: structural and funct
A:Reference number: I54766; MUID:95252184; PMID:7537533
A:Accession: I54766
A:Molecule type: mRNA
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-321 <RES>
A:Cross-references: EMBL:U05593; NID:g453381; PIDN:AAA80154.1; PID:g453382
C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 52.3%; Score 601.5; DB 2; Length 321;
Best Local Similarity 54.4%; Pred. No. 3.6e-41;
Matches 112; Conservative 35; Mismatches 58; Indels 1; Gaps 1;

QY 1 GLSHFCSGVI-HVTKEVKEVATLSCHGNVSVVEELAQTRIIYQKEKKMVLTMMSGDMNIW 59
|||||
Db 31 GLLIQSSGIVGVQSVKREKALLSCDYKFCSEQSIHRIYQKHDKMVLVSVISGVPEVWP 90
|||||

QY 60 EYKNRTIEDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVSKADFTPT 119
|||||
Db 91 KYKNRTVYDIANNYSLLGLILSDRGTTTCVVQRYEGSGYVVKHLTTVVELSVRADFTPT 150
|||||

QY 120 SISDFEIPTSNIIRRICTSGGFPPEHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 179
|||||
Db 151 NITEYGNPSADIKRITCFASGFPKPLSLWLENGLINGINTTISQDPESELYTSSOLD 210
|||||

QY 180 ENMTNHSFMCILIKYGHRLRVNQTNNW 205
|||||
Db 211 FNATYDHFIDCFIEYGDVAHVSNFTW 236
|||||

RESULT 5
I49503
B-lymphocyte activation antigen 7 precursor - mouse
N:Alternate names: MB7-2
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
C:Accession: I49503; S17291; I49521
R:Selvakumar, A.; White, P.C.; Dupont, B.
Immunogenetics 38, 292-295, 1993
A:Title: Genomic organization of the murine B-lymphocyte activation antigen B7.
A:Reference number: I49503; MUID:93307789; PMID:7686531
A:Accession: I49503
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:LJ2589; NID:g293299; PIDN:AAA37240.1; PID:g293301
R:Freeman, G.J.; Gray, G.S.; Glimm, C.D.; Lombard, D.B.; Zhou, L.J.; White, M.; Finge
J. Exp. Med. 174, 625-631, 1991
A:Title: Structure, expression, and T cell costimulatory activity of the murine homol
A:Reference number: S17291; MUID:91341422; PMID:1714935
A:Accession: S17291
A:Molecule type: mRNA
A:Residues: 1-274, 'R', 279-309 <PRE>
A:Cross-references: EMBL:X60958; NID:g50111; PIDN:CAA43291.1; PID:g50112
R:Inobe, M.; Linsley, P.S.; Ledbetter, J.A.; Nagai, Y.; Tamakoshi, M.; Uede, T.
Biochem. Biophys. Res. Commun. 200, 443-449, 1994
A:Title: Identification of an alternatively spliced form of the murine homologue of B
A:Reference number: I49521; MUID:94220123; PMID:7513163

A:Accession: I49521
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-143,238-274,'R',279-309 <RE2>
A:Cross-references: GB:D16220; NID:g505118; PIDN:BAA03748.1; PID:g994769
C:Genetics:
A:Gene: B7
A:Introns: 37/1; 143/1; 237/1; 275/1
A:Superfamily: B-lymphocyte restricted antigen B7
C:Keywords: alternative splicing

Query Match 48.8%; Score 561; DB 2; Length 309;
Best Local Similarity 50.7%; Pred. No. 6.5e-38;
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY 12 VTKVEKVEATLSCGHNVSEELAQTRIVYQKEKKMVLTMMSGDMNIWPEYKKNRTIFDITN 71
DB 42 LSKSVKDKVLLPCRYNSPHEDESDRIYQKHDKVVLVSIAGKLVWPEYKKNRTLYDNT- 100
QY 72 NLSIVILALRPSDEGTVEYVLYKEDAFKREHLAEVTLVSVKADFTPTPSISDFEIPTSNI 131
DB 101 TYSLLITGLVLSDRGYSCVWQKERTYEVKHLALVLSIKADFTPTNITSGNPSADT 160
QY 132 RRICTSGGFPPLHLSWLENGEELNAINTVSQDPETELYAVSSKLDNFMTNTHSFMC 191
DB 161 KRITCFASGGFPKPRFSWLENGELPGINTTISQDPESELYTSSQLDFTNRNHTIKCL 220
QY 192 IKYGLHRLVQNTFNWNTTKQEHFPDN 216
DB 221 IKYGDAHVSEDTWEKPPEDP-PDS 244

RESULT 6
JC7604
CD86 spliced variant CD86 deltaTM isoform - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7604
R:Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeannin, P.; Bonnefoy, J.Y.; Delneste, Y.
Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
A:Title: Identification of an alternatively spliced variant of human CD86 mRNA.
A:Reference number: JC7604; MUID:21092744; PMID:11162656
A:Accession: JC7604
A:Molecule type: mRNA
A:Residues: 1-275 <MAG>
C:Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
C:Genetics:
A:Gene: cd86deltaTM
C:Keywords: immune response

Query Match 16.1%; Score 185; DB 2; Length 275;
Best Local Similarity 27.4%; Pred. No. 1.2e-07;
Matches 165; Conservative 42; Mismatches 78; Indels 52; Gaps 12;

QY 18 EVATLSC---GHNVSVEELAQTRIVYQKEKKMVLTM---SGDMNIWPEYKKNRTIFDI 69
DB 28 ETADLPQCFANSQNSLSLV---VFQDQENLVNEVLGKEKFDVSHSKYMGRTSFD- 83
QY 70 TNNLSIVILALRPSDEGTVEYVLYKEDAFKREHLAEVTLVSVKADFTPTPSISDFEIPTS 129
DB 84 SDSWTLRLHNLQIKDKGLQYIIHKKPTGMIRIHMNSSELSVLANSFQPEI----VPIS 139
QY 130 NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTV-----SQDPETELYAVS 175
DB 140 NITENVYINLTCSHIGYPEPKMSVL-----LRTKNSTIYDGMQKSDQNVTELYDVS 194
QY 176 SKLDF---NMTNHSFMCILIKYGLHRLVQ---TFNWNITKOE-----HFPD 215
DB 195 ISLSVSPDVTNSMTIFCILETDKTRLSSPFSIGTNTMEREESEQTKKREKIHPE 251

RESULT 7
A48754

B7-2 antigen - human
N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48754; S39055
R:Freeman, G.J.; Gribben, J.G.; Boussiotis, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard
Science 262, 909-911, 1993
A:Title: Cloning of B7-2, a CTLA-4 counter-receptor that costimulates human T cell pr
A:Reference number: A48754; MUID:94053735; PMID:7694363
A:Accession: A48754
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-329 <FRE>
A:Cross-references: GB:L25259; NID:g416368; PIDN:AAA58389.1; PID:g416369
A:Note: it is uncertain whether Met-1 or Met-7 is the initiator
R:Azuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza,
Nature 366, 76-79, 1993
A:Title: B70 antigen is a second ligand for CTLA-4 and CD28.
A:Reference number: S39055; MUID:94050123; PMID:7694153
A:Accession: S39055
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 7-329 <AZU>
A:Cross-references: GB:U04343; NID:g439838; PIDN:AAB03814.1; PID:g439839
C:Genetics:
A:Gene: GDB:CD86; CD28LG2
A:Cross-references: GDB:433597; OMIM:601020
A:Map position: 3q13.3-3q21
C:Superfamily: B7-2 antigen
C:Keywords: glycoprotein

Query Match 15.8%; Score 182; DB 1; Length 329;
Best Local Similarity 29.0%; Pred. No. 2.7e-07;
Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;

QY 18 EVATLSC---GHNVSVEELAQTRIVYQKEKKMVLTM---SGDMNIWPEYKKNRTIFDI 69
DB 34 ETADLPQCFANSQNSLSLV---VFQDQENLVNEVLGKEKFDVSHSKYMGRTSFD- 89
QY 70 TNNLSIVILALRPSDEGTVEYVLYKEDAFKREHLAEVTLVSVKADFTPTPSISDFEIPTS 129
DB 90 SDSWTLRLHNLQIKDKGLQYIIHKKPTGMIRIHMNSSELSVLANSFQPEI----VPIS 145
QY 130 NIR-----RIICSTSGGFPEP-HLSWLENGEELNAINTV-----SQDPETELYAVS 175
DB 146 NITENVYINLTCSHIGYPEPKMSVL-----LRTKNSTIYDGMQKSDQNVTELYDVS 200
QY 176 SKLDF---NMTNHSFMCILIKYGLHRLV 199
DB 201 ISLSVSPDVTNSMTIFCILETDKTRL 227

RESULT 8
I49522
gene B7-2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I49522
R:Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Klu
J. Exp. Med. 178, 2185-2192, 1993
A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell
A:Reference number: I49522; MUID:94065585; PMID:7504059
A:Accession: I49522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:L25606; NID:g432478; PIDN:AAA79770.1; PID:g432479
C:Genetics:
A:Gene: B7-2
C:Superfamily: B7-2 antigen

Query Match 13.2%; Score 152; DB 2; Length 309;
Best Local Similarity 26.1%; Pred. No. 6.7e-05;

[illegible]

RESULT 9
I46691
CD86 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 23-Jul-1999
C:Accession: I46691
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecule
A:Reference number: I46689; MUID:95369849; PMID:7642234
A:Accession: I46691
A>Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-330 <ISO>
A:Cross-references: GB:D49842; NTD:g755098; PIDN:BAA08642.1; PID:g755099
C:Superfamily: E7-2 antigen

Query Match	12.3%	Score 140.5;	DB 2;	Length 330;
Best Local Similarity	27.4%;	Pred. No. 0.00061;		
Matches	60;	conservative 34;	Mismatches 84;	Indels 41; Gaps 12;
QY	18	EVATSLGCH-NVSVEEELAQRIYQWEKKAVLTMM-----SGDMNIWPEYKNTTIFDTN- 71		
Db	34	KTADLPQFTNSQSRSLSELVWFQDERLVLFGLGREKPDNDPKYIGTSTFDESW 93		
QY	72	NLSIVILALRPSDEGYECVVLKYEKDAFKREHLAEVTLVSKADPPTPSIDFETPSNI 131		
Db	94	NQLHNVQIK--DKGYQCFVHHGAKGLPIYQMNSLSVLANFTQPEIT-----LISNI 147		
QY	132	RR-----IICSTGGGPEPHLSWLENCEELNNTTV-----SDPETELY--AVSS 176		
Db	148	TRNSAINLACSSVQGGPEPKMFF---VLKTNATTEYDGVTEKSDQNVTLGYNISISG 203		
QY	177	KLDF-NWTTNHSFCLIKYGHLRVNQTFNNTTKQEHFP 214		
Db	204	STTFSDDIRNATLYCVL-----GTESPEYTSO-HFP 233		

RESULT 10
I39428
a1cam - human
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1995 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I39428
J:Bowen, M.A.; Patel, D.D.; Li, X.; Modrell, B.; Malacko, A.R.; Wang, W.C.; Marguardt, H.
J. Exp. Med. 181, 2213-2220, 1995
A:Title: Cloning, mapping, and characterization of activated leukocyte-cell adhesion mol
A:Reference number: I39428; MUID:95279947; PMID:7760007
A:Accession: I39428
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-383 <RES>
A:Cross-references: GB:I38608; NID:g886257; PIDN:AAB59499.1; PID:g886258

Query Match	11.6%	Score 133.5;	DB 2;	Length 583;
Best Local Similarity	24.5%;	Pred. No. 0.0046;		
Matches	37;	Conservative	35;	Mismatches 54;
				Indels 25;
Gaps				
Qy	59	PEYNRRIFDITNNLSIVIALRPSDEGTYECVLYKEDAKREHLAEVTLISVRADPFT	118	
		: : : : : : : : : : : : : : :		
Db	84	PEYKDR--LNLSENYTISISNAKISDEKRVCLMVT--EDNVFEAPTIVKV-----FKQ	133	
		: : : : : : : : : : : : : : :		
Qy	119	PSISDFE-----IPTSNIKKI--ICSTSGGPPPEHLKSWLENGEELNAINTV-----SOD	166	
		: : : : : : : : : : : : : : :		
Db	134	PSKPEIVSKALFETEQLLKGLDCISDSYDGNITWYRNGKVLHPLGAVIIFKEMD	193	
		: : : : : : : : : : : : : : :		
Qy	167	PETELYAVSSKLDPNMT---TNHSFMCLIKY	194	
		: : : : : : : : : : : : : : :		
Db	194	PVTQLYTMWTSTLEYKTKKADIQMPFTCSVTY	224	
		: : : : : : : : : : : : : : :		
RESULT 11				
QOQB48				
BARR1	protein - human herpesvirus 4 (strain B95-8)			
C:Species:	human herpesvirus 4, Epstein-Barr virus			
C:Date:	25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1990			
C:Accession:	B43045; A03792; S33058			
R:Banker,	A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.			
Mol. Biol. Med.	1, 21-45, 1983			
A:Title:	Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus genome			
A:Reference number:	A93065; MUID:85035713; PMID:6092825			
A:Accession:	B43045			
A:Molecule type:	DNA			
A:Residues:	1-221 <BAN>			
A:Cross-references:	EMBL:V01555; NID:g59074; PIDN:CAA24809.1; PID:g1334917			
R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; G.				
Nature	310, 207-211, 1984			
A:Title:	DNA sequence and expression of the B95-8 Epstein-Barr virus genome			
A:Reference number:	A03794; MUID:84270867; PMID:6087149			
A:Contents:	annotation; protein coding region			
C:Superfamily:	human herpesvirus 4 BARR1 protein			

RESULT 11

QCB548

BARF1 protein - human herpesvirus 4 (strain B95-8)

C:Species: human herpesvirus 4, Epstein-Barr virus

C:Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999

C:Accession: B43045; A03792; S33058

R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Bartell, B.G.

Mol. Biol. Med. 1, 21-45, 1983

A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr v1

A:Reference number: A93065; MUID:85035713; PMID:6092825

A:Accession: B43045

A:Molecule type: DNA

A:Residues: 1-221 <BAN>

A:Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24809.1; PID:g1334917

R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; Nature 310, 207-211, 1984

A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.

A:Reference number: A03794; MUID:84270667; PMID:60871149

A:Contents: annotation; protein coding region

C:Superfamily: human herpesvirus 4 BARF1 protein

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Query Match      11.2%; Score 129; DB 1; Length 221;
Best Local Similarity 27.0%; Pred. No. 0.0031;
Matches 43; Conservative 25; Mismatches 47; Indels 44; Gaps 8;

QY      18 EVATLSCGHNVSVVELAQTRIYWQK-----EKKWVLTMSSGDMNIWPE 60
      : | | | | | | | | | | | | | | | | | | | | | | | |
Db      19 QAVTAFGLGERVTLTS-----IWRVSLGPIEIVSWFKLGPGEQVLTRMHHDV-IFIE 71
      : | | | | | | | | | | | | | | | | | | | | | | | |

QY      61 YKNRTIFDI---TNNSIVILALPSPDEGTCECVVLKYKDAFKRHLAEV---TLSV-- 112
      : | | | | | | | | | | | | | | | | | | | | | | | |
Db      72 WPPRGFDIHRSAFTFLVYTAANISHDGNVLCRMKLGETEVTQKHLHSVVKPLTSLSVHS 131
      : | | | | | | | | | | | | | | | | | | | | | | | |

QY      113 -KADFPPTSIDFPIPTSNIRRIICSTSGGPEPHLSWL 150
      : | | | | | | | | | | | | | | | | | | | | | | | |
Db      132 ERSQFP-----DFSLT-----VTCRVNAPPHPHVOWL 159
      : | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 12

S70587
butyrophilin precursor - human
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C:Accession: S70587
R:Taylor, M.R.; Peterson, J.A.; Ceriani, R.L.; Couto, J.R.
Biochim. Biophys. Acta 1306, 1-4, 1996
A:Title: Cloning and sequence analysis of human butyrophilin reveals a potential rece
A:Reference number: S70587; MUID:96201696; PMID:8611614
A:Accession: S70587
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-526 <TAG>
A:Cross-references: EMBL:U39576; NID:g1326082; PID:AA050489.1; PID:g1326083

Query Match 11.1%; Score 127; DB 2; Length 526;
Best Local Similarity 27.5%; Pred. NO. 0.014;

Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps 10;

Qy 16 VKEVATLSC--GHNVSVEELAQTRIIYWOKEKKMVLTMMSG---DNIIWPEYKNRTIF--- 67

Db 42 VGEDAELPCRLSPNASEHL-ELRWRKKVSPAVLVHRDGRQEAEQMPYRGRATLVQD 100

Qy 68 -DITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFTPTSDPEI 126

Db 101 GIAGRVALRGRVSDGTYCF--FREDGSYEAL--VHLKVAALGSDPHIS-MQV 154

Qy 127 PTSNRIICSTSGGFPPEHLSW-LENGEELNAINITVTSQDPETE-LYAVSSKLDNFMTT 184

Db 155 QENGICIECTSVGVPEPQVQWRTSKGKPP--STSESNPDEGLTVAASVIIRDT 212

Qy 185 NHPFMCLIK 193

Db 213 TKNVSCYIQ 221

RESULT 13

JH0506

adhesion molecule SCL precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000

C:Accession: JH0506; PS0270

R:Yanaka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.; Kohr, B.;

Neuron 7, 535-545, 1991

A:Title: Molecular cloning and expression of a novel adhesion molecule, SCL.

A:Reference number: JH0506; MUID:92030150; PMID:1931049

A:Accession: JH0506

A:Molecule type: mRNA

A:Residues: 1-588 <TAN>

A:Cross-references: GB:S63276; MID:g238000; PIDN:AAB20170.1; PID:g238001

A:Experimental source: embryo

A:Accession: PS0270

A:Molecule type: protein

A:Residues: 34-48 <TANI>

C:Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons

C:Keywords: glycoprotein; transmembrane protein

F:1-33/Domain: signal sequence status predicted <STG>

F:34-588/Product: adhesion molecule SCL #status predicted <ADH>

F:500-523/Domain: transmembrane #status predicted <TRA>

F:101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 10.7%; Score 122.5; DB 2; Length 588;

Best Local Similarity 25.7%; Pred. No. 0.036;

Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

Qy 59 PEYKNTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFTPT 118

Db 90 PDYKDR--LSLSNYTILSKNARISDEKRFVCMVLT-EDDVSEPTVVKV-----FKQ 139

Qy 119 PS-----ISDPEIPTSNIIRI-ICSTSGGFPPEHLSWLENG-----EELNAINITVTSQ 165

Db 140 PSQPEILHQADF-LETEKLMKCEVVRSDYPEGNTWYKNGRVLPQVEEVVILNRKVE 198

Qy 166 DPTELYAVSSKLDNFMT---TNHSPMCLIKY 194

Db 199 NRSTGLFTMTSSLOYMPTKEDANAKFTCIVTY 230

RESULT 14

A45254

surface glycoprotein BEN precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jul-2000

C:Accession: A45254; S19202

R:Pourquie, O.; Corbel, C.; Le Caer, J.P.; Rossier, J.; Le Douarin, N.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 5261-5265, 1992

A:Title: BEN, a surface glycoprotein of the immunoglobulin superfamily, is expressed in

A:Reference number: A45254; MUID:92302224; PMID:1608932

A:Accession: A45254

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-588 <POU>

A:Cross-references: EMBL:X64301; NID:g63087; PIDN:CAA45579.1; PID:g63088

C:Keywords: glycoprotein

Query Match 10.7%; Score 122.5; DB 2; Length 588;

Best Local Similarity 25.7%; Pred. No. 0.036;

Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

Qy 59 PEYKNTIFDITNNLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFTPT 118

Db 90 PDYKDR--LSLSNYTILSKNARISDEKRFVCMVLT-EDDVSEPTVVKV-----FKQ 139

Qy 119 PS-----ISDPEIPTSNIIRI-ICSTSGGFPPEHLSWLENG-----EELNAINITVTSQ 165

Db 140 PSQPEILHQADF-LETEKLMKCEVVRSDYPEGNTWYKNGRVLPQVEEVVILNRKVE 198

Qy 166 DPTELYAVSSKLDNFMT---TNHSPMCLIKY 194

Db 199 NRSTGLFTMTSSLOYMPTKEDANAKFTCIVTY 230

RESULT 15

JC5288

SHP substrate-1 protein, 509 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Apr-1997 #sequence_revision 09-May-1997 #text_change 20-Jun-2000

C:Accession: JC5288

R:Yanaka, H.; Matsui, T.; Agata, A.; Tomura, M.; Kubota, I.; McFarland, K.C.; Kohr, B.;

Neuron 7, 535-545, 1991

A:Title: Molecular cloning and expression of a novel adhesion molecule, SCL.

A:Reference number: JH0506; MUID:92030150; PMID:1931049

A:Accession: JH0506

A:Molecule type: mRNA

A:Residues: 1-588 <TAN>

A:Cross-references: GB:S63276; MID:g238000; PIDN:AAB20170.1; PID:g238001

A:Experimental source: embryo

A:Accession: PS0270

A:Molecule type: protein

A:Residues: 34-48 <TANI>

C:Comment: This protein is uniquely and transiently expressed on spinal cord motoneurons

C:Keywords: glycoprotein; transmembrane protein

F:1-33/Domain: signal sequence status predicted <STG>

F:34-588/Product: adhesion molecule SCL #status predicted <ADH>

F:500-523/Domain: transmembrane #status predicted <TRA>

F:101,173,199,271,312,366,462,485,504/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 10.5%; Score 120.5; DB 2; Length 509;

Best Local Similarity 25.9%; Pred. No. 0.044;

Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

Qy 3 SHFCSGV---IHVTKEVKEVA-----TLCGHNVSVEELAQTRIIYWK---EKKMVL 48

Db 23 SCFTGVTGKELKVTQPEKSVVAAGDSTVLC---TLTSLLPVGPVKWYRGVQGSRLLI 79

Qy 49 TMMSGDMNIWPEYKNRTIFDIT--NNL--SIVILALRPSDEGTVECVLKYKDAFKREH 104

Db 80 YSTGEH--FPRVTN--VSDATKRNNDMSIRISNVTPEADAGTYCV--KFQKGPSPDT 133

Qy 105 L-----AEVTLVKADFTPTPS-ISDPEIPTSNIIRIICSTSGGFPPEHLSWLENGEEL 156

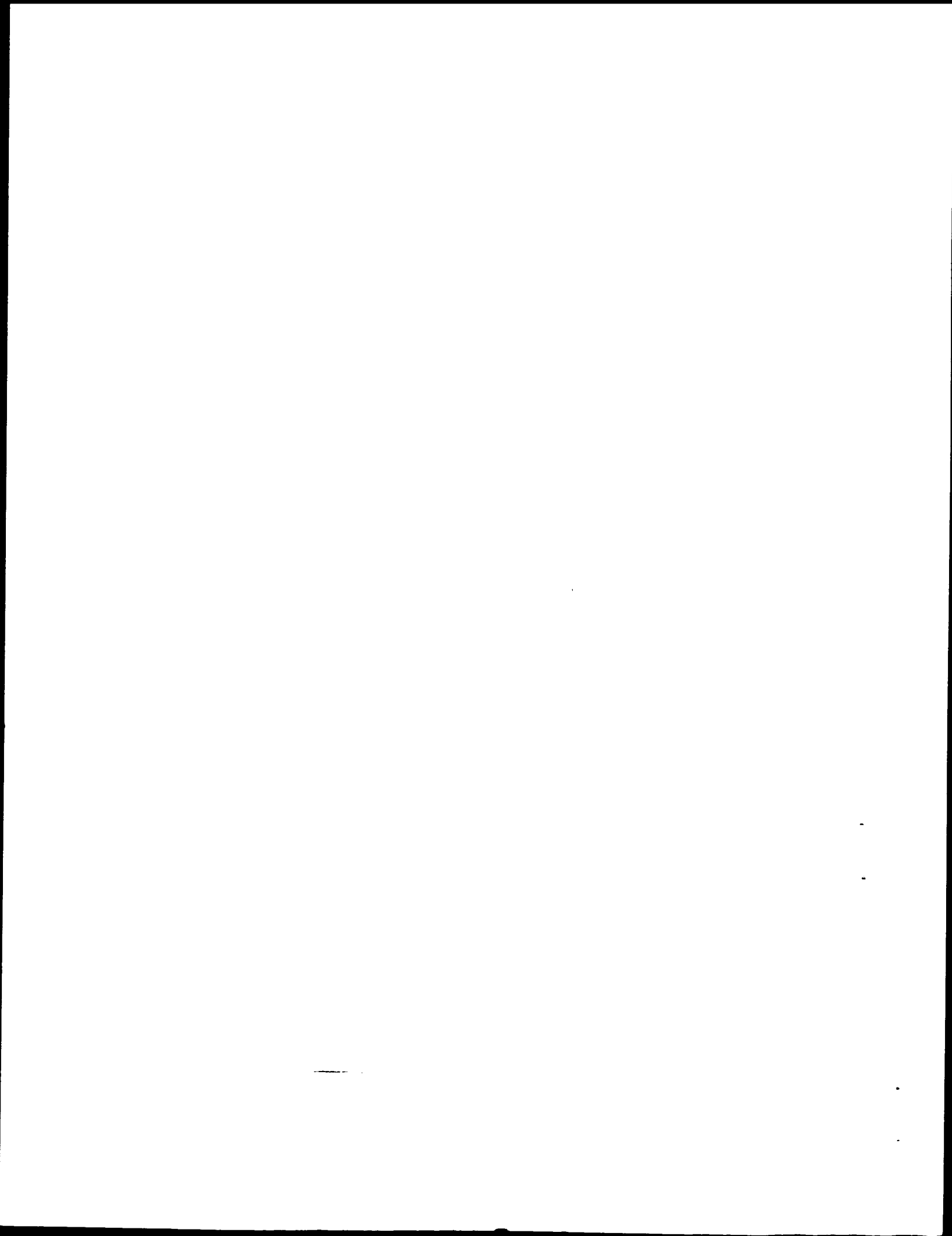
Db 134 EIQSGGTEVYVLAKPSPPEVSGPADRGIPQKV-NETCKSHGFSRNTILKFKDQDEL 192

Qy 157 NAINTVTSQDPTELYAVSS--KLDNFMTTNHSPMCLIKYKHLRVNOT 202

Db 193 HHLETTVPNGKNVSNYISSTVTVVLNMDVHS--KVCEVAHITLDRS 239

Search completed: January 6, 2003, 14:25:30

Job time : 23 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:20:25 ; Search time 13 Seconds

(without alignments)
689.145 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVIHVKREKVA.....LRVNTQFNWNTKQEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	1 CD80_HUMAN	P33681 homo sapien
2	738	64.2	299	1 CD80_RABIT	P42070 oryctolagus
3	561	48.8	306	1 CD80_MOUSE	Q00609 mus musculus
4	182	15.8	329	1 CD86_HUMAN	P42081 homo sapien
5	161	14.0	302	1 ICOL_HUMAN	O75144 homo sapien
6	152	13.2	309	1 CD86_MOUSE	P42082 mus musculus
7	150.5	13.1	322	1 ICOL_MOUSE	Q9JHJ8 mus musculus
8	140.5	12.2	330	1 CD86_RABIT	P42071 oryctolagus
9	134.5	11.7	583	1 C166_MOUSE	Q61490 mus musculus
10	133.5	11.6	583	1 C166_HUMAN	Q13740 homo sapien
11	129	11.2	221	1 BREL_EBV	P03228 Epstein-bar
12	127	11.1	526	1 BURY_HUMAN	Q13410 homo sapien
13	122.5	10.7	588	1 C166_CHICK	P42292 gallus gall
14	119	10.4	524	1 BURY_MOUSE	Q62556 mus musculus
15	116.5	10.1	1088	1 NCA1_XENLA	P16170 xenopus lae
16	115	10.0	761	1 NCA2_HUMAN	P13592 homo sapien
17	115	10.0	848	1 NCA1_HUMAN	P13591 homo sapien
18	110.5	9.6	321	1 TCE_FLY	P11364 feline leuk
19	109.5	9.5	646	1 M018_HUMAN	P43121 homo sapien
20	109.5	9.5	853	1 NCA1_BOVIN	P31836 bos taurus
21	109	9.5	526	1 BURY_BOVIN	P18892 bos taurus
22	109	9.5	2029	1 LAR_DROME	P16521 drosophila
23	108.5	9.4	365	1 CXAR_MOUSE	P97792 mus musculus
24	107.5	9.4	333	1 AMAL_DROME	P15364 drosophila
25	106.5	9.3	858	1 NCA1_RAT	P13596 rattus norv
26	105	9.1	319	1 A33_HUMAN	Q99795 homo sapien
27	105	9.1	1091	1 NCA1_CHICK	P13590 gallus gall
28	104	9.1	1092	1 NCA2_XENLA	P36335 xenopus lae
29	103.5	9.0	725	1 NCA2_MOUSE	P13594 mus musculus
30	103.5	9.0	1115	1 NCA1_MOUSE	P13595 mus musculus
31	103	9.0	298	1 JAM2_HUMAN	P57087 homo sapien
32	102	8.9	1443	1 NEOL_CHICK	Q90610 gallus gall
33	101.5	8.8	403	1 RAGE_MOUSE	Q62151 mus musculus

ALIGNMENTS

RESULT 1

ID	CD80_HUMAN	STANDARD;	PRT;	288 AA.
AC	P33681:			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DE	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (CTLA-4 counter-receptor B7.1) (B7) (BBI).			
GN	CD80 OR CD28LG1 OR CD28LG OR LAB7.			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
TX	TISSUE=Lymphoid;			
RX	MEDLINE=90010147; PubMed=2794510;			
RA	Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F., Nadler L.M.;			
RT	"B7, a new member of the Ig superfamily with unique expression on activated and neoplastic B cells."			
RL	J. Immunol. 143:2714-2722(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92307753; PubMed=1377173;			
RA	Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.;			
RT	"Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7."			
RL	Immunogenetics 36:175-181(1992).			
RN	[3]			
RP	SEQUENCE OF 35-38.			
RX	MEDLINE=91341422; PubMed=1714935;			
RA	Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J., White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;			
RT	"Structure, expression, and T cell costimulatory activity of the murine homolog of the human B lymphocyte activation antigen B7."			
RL	J. Exp. Med. 174:625-631(1991).			
RN	[4]			
RP	CHARACTERIZATION.			
RX	MEDLINE=95088403; PubMed=7527824;			
RA	Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.;			
RT	"CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL."			
RL	J. Immunol. 154:97-105(1995).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.			
RX	MEDLINE=20125021; PubMed=10661405;			
RA	Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K., Jones E.Y., Stuart D.I., Davis S.J.;			
RT	"Structure and dimerization of a soluble form of B7-1."			
RL	Immunity 12:51-60(2000).			
CC	-I- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE			

P31398 manduca sex
P17948 h vascular
P78310 homo sapien
Q9qxs7 mus musculus
P04218 rattus norv
Q9xt56 bos taurus
P35969 mus musculus
P53767 rattus norv
P19320 homo sapien
Q9r044 rattus norv
P40199 homo sapien
P12960 mus musculus

34 100 8.7 413 1 HEMO_MANSE
35 99.5 8.7 1338 1 VGR1_HUMAN
36 98.5 8.6 365 1 CXAR_HUMAN
37 98.5 8.6 1242 1 NPHN_MOUSE
38 98 8.5 278 1 OX2G_RAT
39 98 8.5 298 1 JAM1_BOVIN
40 98 8.5 1333 1 VGR1_MOUSE
41 97 8.4 1336 1 VGR1_RAT
42 96.5 8.4 739 1 VCAL_HUMAN
43 96.5 8.4 1234 1 NPHN_RAT
44 96 8.4 344 1 CEAG_HUMAN
45 96 8.4 1020 1 CONT_MOUSE

QY 4 HFCSGVHTVKEVATLSCGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPEYKN 63
 Db 29 HFSGIGSVTKSVKEMALSDYNISDELARMRIYQKQDMYLSISGQVEVWPEYKN 88
 QY 64 RTIFDITNNLSIVTLALRPSDEGYECVWLKYEDAFKREHLAEVTLVKADFPPTPSISD 123
 Db 89 RTFFDITNNLSMLALRLSDKGYTCVQKNENGSPREHLTSVTLISIRADFPVPSITD 148
 QY 124 FEIPTSNNIRICSTGGFPPLHLSWLENGEELNAINTVSQDPETELYAVSSKLDNFMT 183
 Db 149 IGHDPNPKVIRCSASGSGFPPLRLAWEDGELNAINTVSQDPETELYAVSSKLDNFMT 208
 QY 184 TNHSPMCLIKYGLRVNQTNNWTKOE 211
 Db 209 NNHSIVCLIKYGLSVSQIFPWSKPQE 236

RESULT 3
 CD80_MOUSE STANDARD; PRT; 306 AA.
 AC Q00609;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (B7).
 DE CD80 OR B7.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=91341422; PubMed=1714935;
 RA Gray G.S., Freeman G.J., Glimi C.D., Lombard D.B., Zhou L.J.,
 RA White M., Fingerioth J.D., Gribben J.G., Nadler L.M.;
 RT "Structure, expression, and T cell costimulatory activity of the
 RT murine homologue of the human B lymphocyte activation antigen B7."
 RL J. Exp. Med. 174:625-631(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=93307789; PubMed=7686531;
 RA Selvakumar A., White P.C., Dupont B.;
 RT "Genomic organization of the mouse B-lymphocyte activation antigen
 RT B7."
 RL Immunogenetics 38:292-295(1993).
 CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
 CC INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
 CC MALIGNANTIES.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
 CC ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
 CC IT'S EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -----
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 CC -----
 CC EMBL; X60958; CAA43291.1; -.

DR EMBL; L12589; AAA37240.1; ALT SEQ.
 DR EMBL; L12585; AAA37240.1; JOINED.
 DR EMBL; L12586; AAA37240.1; JOINED.
 DR EMBL; L12587; AAA37240.1; JOINED.
 DR EMBL; L12588; AAA37240.1; JOINED.
 DR PIR; S17291; S17291.
 DR HSP; P33681; 1DR9.
 DR MGD; MGI:101775; CG80.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00410; IG_like; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 37
 FT CHAIN 38 306
 FT DOMAIN 38 246
 FT TRANSMEM 247 268
 FT DOMAIN 269 306
 FT DOMAIN 47 126
 FT DOMAIN 158 226
 FT DOMAIN 227 246
 FT DISULFID 54 119
 FT DISULFID 165 219
 FT CARBOHYD 93 93
 FT CARBOHYD 99 99
 FT CARBOHYD 149 149
 FT CARBOHYD 189 189
 FT CARBOHYD 210 210
 FT CARBOHYD 214 214
 SQ SEQUENCE 306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;

Query Match 48.8%; Score 561; DB 1; Length 306;
 Best Local Similarity 50.7%; Pred. No. 4.1e-40;
 Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY 12 VTKEVKEVATLSCGHNVSVEELAQTRIVYQKEKKVLTMMSGDMNIWPEYKNRTIFDITN 71
 Db 42 LSKSVKDKVLLPCRYNSPHEDESDRIYQKHDKVLSVIAGKLVKWPVEYKNRTLYDNT- 100
 QY 72 NLSIVILALRPSDEGYECVWLKYEDAFKREHLAEVTLVKADFPPTPSISDEIFTSNI 131
 Db 101 TYSILILGLVLSDRGTYSVCVQKRGTYEVKHLALVKLSIKADSFSTPNITSGNPSADT 160
 QY 132 RRIICSTGGFPPLHLSWLENGEELNAINTVSQDPETELYAVSSKLDNFMTNHSFMC 191
 Db 161 KRITCFASGGFPKPRFSLWLENGRELPGINTTISQDPSELYTSSQLDFTNTHTIKCL 220
 QY 192 IKYGLRVNQTNNWTKOEHPDN 216
 Db 221 IKYGAHVSEDFTWEKPPDP-PDS 244

RESULT 4
 CD86_HUMAN STANDARD; PRT; 329 AA.
 AC P42081; Q13655;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE T lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen) (CTLA-4 counter-receptor B7.2) (B70) (FUN-1) (BU63).
 DE CD86 OR CD28LG2.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=94053735; PubMed=7694363;
 RX Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,

RL Patent number WO0121796, 29-MAR-2001.
 CC -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
 CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
 CC TH2 PHENOTYPE.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
 CC (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY
 CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND Peyer's
 CC PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
 CC CELLS. T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
 CC -!- DEVELOPMENTAL STAGE: DETECTED EARLY IN HEMOPOIESIS: IN THE YOLK
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
 CC 14.5 DPC.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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 DR EMBL; AF216747; AAF45149.1; -
 DR EMBL; AF199027; AAF34738.1; -
 DR EMBL; AX100591; CAC36463.1; -
 DR EMBL; AX100593; CAC36464.1; -
 DR EMBL; AF394451; AAK7544.1; -
 DR MGD; MGI:1354701; Icosl.1.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00409; Ig; 1.
 DR SMART; SM00410; Ig_Like; 1.
 DR B-cell activation; Immune response; Glycoprotein;
 KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 KW Alternative splicing.
 FT SIGNAL 1 46
 FT CHAIN 47 322
 FT DOMAIN 47 277
 FT DOMAIN 278 298
 FT TRANSMEM 299 322
 FT DOMAIN 55 145
 FT DOMAIN 178 250
 FT DOMAIN 31 38
 FT DOMAIN 289 292
 FT DISULFID 62 138
 FT DISULFID 185 243
 FT CARBOHYD 71 71
 FT CARBOHYD 120 120
 FT CARBOHYD 163 163
 FT CARBOHYD 200 200
 FT CARBOHYD 213 213
 FT CARBOHYD 252 252
 FT CARBOHYD 265 265
 FT VARSPLIC 321 322
 FT ISOFORM 2).

FT CONFLICT 237 237 R -> H (IN REF. 4 AND 5; CAC36464).
 SQ SEQUENCE 322 AA; 35960 MW; 55CCBA4AD12E47E6 CRC64;
 Query Match 13.1%; Score 150.5; DB 1; Length 322;
 Best Local Similarity 27.1%; Pred. No. 1.4e-05;
 Matches 65; Conservative 32; Mismatches 102; Indels 41; Gaps 12;
 QY 2 LSHFC--SGVHVHTKVKVAVATLSGCHNYSVE-----ELAQRIYQKEKMW-----L 48
 DB 38 LSLCAASAEETEGAMVGSNVVLSG-----IDPHRHFNLSGLYVYVWQENPEVSYYL 92
 QY 49 TMSGDMWPEYKGNRTIFDITN-----NLSIVILALRPDSGTYECVWLKYEKDAFKRH 104
 DB 93 PYKSPGINDSSYKNGHLSLDSMKQGNFSYLNKNTVPDQTQFTCRV--FMNTATELVK 150
 QY 105 LAE--VTLVSKADFPFP--SISDFEPTNIRRIICSTSGGFPPEPHLSWLENGEELNAIN 160
 DB 151 ILEEVYRLRVAANFSPVISTSDSNPGQE--RTYTCMSKNGYPEPNLYWT--NTDNLSD 208
 QY 161 TTVSQDP---ETELVAVSKLDFNMTNHSFMCLIKYHGLRVN-----QTFNWNNTTK 209
 DB 209 TALQNTVYLNKLGLDVISTLRLPWTSGDVLCCVENVALHQNITISISQAESFTGNNTK 268
 RESULT 8
 CD86_RABIT STANDARD; PRT; 330 AA.
 ID CD86_RABIT
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
 DE antigen).
 GN CD86.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHBB:HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules";
 RL Immunogenetics 42:217-220(1995).
 CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
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 CC
 CC EMBL; D49842; BAA08642.1; -
 CC InterPro; IPR003006; Ig_MHC.
 CC InterPro; IPR003596; Ig_v.
 CC SMART; SM00406; Ig_v; 1.
 CC PROSITE; PS00290; Ig_MHC; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 330 B LYMPOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN 23 247 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 248 268 POTENTIAL.
FT DOMAIN 269 330 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 117 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 150 225 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 110 POTENTIAL.
FT DISULFID 157 218 POTENTIAL.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 330 AA; 37142 MW; 935CDD65C57E3EE1 CRC64;

Query Match 12.2%; Score 140.5; DB 1; Length 330;
Best Local Similarity 27.4%; Pred. No. 9.7e-05;
Matches 60; Conservative 34; Mismatches 84; Indels 41; Gaps 12;

QY 18 EVATLSGCH-NVSYEEAQAQRIYQKQKMLVTMM-----SGDMNIWPEYKNTIFDITN- 71
DB 34 KTADLPQFTNSQSRSELVFWQDQGRVLYELFLGRKPDNDPKYIGRTSFDQSW 93

QY 72 NLSVILALRPSDEGTVECVLVKYEKDAFKREHLAEVLSVKADPPTPSISDFEPTSI 131
DB 94 NLQHNVOIK--DKGVYQCFVHHRGAKGLVPIYQMNSELVLANFTQPEIT---LISNI 147

QY 132 RR-----IICSTSGGPPPHLSWENGEELNAINTV-----SQDPETELY--AVNS 176
DB 148 TRNSAINLTCSSVQGYPEPKMKFF---VLKTENATTEYDGVIERKSDQNVNGLYNISIG 203

QY 177 KLDP-NMTTNSFMCILIKYGLHVRNVTENWNTKQEHPP 214
DB 204 SITFSDOIRNATYICVL-----QTESTETYSQ-HPP 233

RESULT 9
C166_MOUSE STANDARD; PRT; 583 AA.
AC Q61490; 070136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE C166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE (ALCAM) (DM-GRASP protein).
GN ALCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NFS;
RX MEDLINE=97353242; PubMed=9209500;
RA Bowen M.A., Bajorath J., D'Elidio M., Whitney G.S., Palmer D.,
RA Kobarg J., Starling G.C., Siadak A.W., Aruffo A.,
RT "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
RT conserved in different homologs and mediates cross-species binding.";
RL Eur. J. Immunol. 27:1469-1478(1997).
RN [2]
RN SEQUENCE OF 227-583 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=94376084; PubMed=6089660;
RA Kanki J.P., Chang S., Kuwada J.Y.;
RT "The molecular cloning and characterization of potential chick
RT DM-GRASP homologs in zebrafish and mouse.";
RL J. Neurobiol. 25:831-845(1994).
CC -/- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6, INVOLVED IN
CC NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO

CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC THE NERVOUS SYSTEM.
CC -/- SUBCELLULAR LOCATION: Type I membrane protein.
CC -/- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -/- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -/- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; U95030; AAC06342.1; -;
DR EMBL; L25274; AAA37528.1; -;
DR HSSP; Q13740; IKJC.
DR MGD; MGI:1313266; Alcam.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00410; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
DR Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Repeat; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 583 CD166 ANTIGEN.
FT DOMAIN 28 527 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 528 549 POTENTIAL.
FT DOMAIN 550 583 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 36 120 IG-LIKE V-TYPE DOMAIN 1.
FT DOMAIN 263 321 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 347 399 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 428 492 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFID 43 113 POTENTIAL.
FT DISULFID 157 220 POTENTIAL.
FT DISULFID 270 313 POTENTIAL.
FT DISULFID 354 392 POTENTIAL.
FT DISULFID 435 485 POTENTIAL.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 227 232 PSQKT -> AAGIPA (IN REF. 2).
FT CONFLICT 454 454 S -> F (IN REF. 2).
SQ SEQUENCE 583 AA; 65161 MW; E7BAFA8FCA8F9489 CRC64;

Query Match 11.7%; Score 134.5; DB 1; Length 583;
Best Local Similarity 25.2%; Pred. No. 0.00063;
Matches 38; Conservative 34; Mismatches 54; Indels 25; Gaps 7;

QY 59 PEYKNTIFDTNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVLSVKADPPT 118
DB 84 PEYKDR--LSLSENITUSIANAKISDEKRFVCMVLT-EDNVFEAPTLVKV-----PKQ 133

QY 119 PSISDFE-----IPTSNIRRI-ICSTSGGFPPEPHLSWENGEELNAINTVS-----QD 166
DB 134 PSKPEIVNKAPFLETDLQKLGDCISRDSYDGNITWTYRNGKVLQPVGEVAILPKKEID 193

QY 167 PETELXAVSSKLDNFNMTNH---SFMCLIKY 194
DB 194 PGQLTIVTSLSLEYKTKTRSDIQMPFTCSVTY 224

RESULT 10
C166_HUMAN

ID C166_HUMAN STANDARD; PRT; 583 AA.
AC Q13740; O60892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CD166 antigen precursor (Activated leukocyte-cell adhesion molecule) (ALCAM).
DE NCBI_TaxID=9606;
GN ALCAM OR MEMD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=95279947; PubMed=7760007;
RA Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R., Francke U., Wang W.-C., Marquardt H., Neubauer M., Pesando J.M., Haynes B.F., Aruffo A.;
RA "Cloning, mapping, and characterization of activated leukocyte-cell adhesion molecule (ALCAM), a CD6 ligand.";
RL J. Exp. Med. 181:2213-2220(1995).
RN [2]
RP SEQUENCE OF 2-583 FROM N.A.
RX MEDLINE=98161527; PubMed=9502422;
RA Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J., van Kooyk Y., Bloemers H.P., Swart G.W.;
RA "MEMD, a new cell adhesion molecule in metastasizing human melanoma cell lines, is identical to ALCAM (activated leukocyte cell adhesion molecule).";
RL Am. J. Pathol. 152:805-813(1998).
RN [3]
RP CD6-BINDING DOMAINS.
RX MEDLINE=96420463; PubMed=8823162;
RA Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.;
RA "Recognition of diverse proteins by members of the immunoglobulin superfamily: delineation of the receptor binding site in the human CD6 ligand ALCAM.";
RL Biochemistry 35:12287-12291(1996).
RN [4]
RP 3D-STRUCTURE MODELING OF 28-133.
RX MEDLINE=96060095; PubMed=8520490;
RA Bajorath J., Bowen M.A., Aruffo A.;
RA "Molecular model of the N-terminal receptor-binding domain of the human CD6 ligand ALCAM.";
RL Protein Sci. 4:1644-1647(1995).
CC -1- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF THE NERVOUS SYSTEM.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD166 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd166.htm".
CC -----
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CC -----
DR EMBL; L38608; RA059499.1; -;
DR EMBL; Y10183; CAA71256.1; -;
DR PDB; 1KJC; 03-APR-96.
DR Genew; HGNC:400; ALCAM.
DR MIM; 601662; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003600; Ig_like.

DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; IG; 2.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW Cell adhesion; immunoglobulin domain; glycoprotein; Transmembrane; CD166 antigen precursor (Activated leukocyte-cell adhesion molecule).
FT SIGNAL 1 27
FT CHAIN 28 583
FT CD166 ANTIGEN.
FT DOMAIN 28 527
FT TRANSMEM 528 549
FT DOMAIN 550 583
FT DOMAIN 36 120
FT DOMAIN 150 227
FT DOMAIN 263 321
FT DOMAIN 347 399
FT DOMAIN 428 492
FT DISULFID 43 113
FT DISULFID 157 220
FT DISULFID 270 313
FT DISULFID 354 392
FT DISULFID 435 485
FT CARBOHYD 91 91
FT CARBOHYD 95 95
FT CARBOHYD 167 167
FT CARBOHYD 265 265
FT CARBOHYD 306 306
FT CARBOHYD 361 361
FT CARBOHYD 457 457
FT CARBOHYD 480 480
FT CARBOHYD 499 499
FT VARIANT 258 258
FT VARIANT 301 301
FT VARIANT M -> T.
FT /FTid=VAR_003907.
SQ SEQUENCE 583 AA; 65132 MW; E023FB974A60284 CRC64;
Query Match 11.6%; Score 133.5; DB 1; Length 583;
Best Local Similarity 24.5%; Pred. No. 0.00076;
Matches 37; Conservative 35; Mismatches 54; Indels 25; Gaps 7;
QY 59 PEYKNRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKRHLAEVTLVSKADPPT 118
DB 84 PEYKDR--LNLSENYTLISNARISDEKRFVCMVLT--EDNVFEAPTIVKV-----FKQ 133
QY 119 PLSIDFE-----IPTSNIIRI--ICSTSGGFPPEPHLSWLENGEELNAINTVT-----SQD 166
DB 134 PSKEIVSKALFTELEQKLKGLDCISDSYDGNITWIRNGKVLHPLEGAVVILFKKMD 193
QY 167 PETELYAVSSKLDNFMT---TNHSFMCLIKY 194
DB 194 PVTQLYTMSTLEYKTKKADIQMPETCSVTY 224
RESULT 11
ID BRFL_EBV
ID BRFL_EBV STANDARD; PRT; 221 AA.
AC P03228;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 33 kDa early protein (p33).
GN BARF1.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Sequin C., Tuffnell P.S., Barrell B.G.;
RA "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RT

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RL Nature 310:207-211(1984).
RN [2]
RP IDENTIFICATION OF PROTEIN.
RX MEDLINE=90059873; PubMed=2555151;
RA Wei M.X., Ooka T.;
RT "A transforming function of the BARF1 gene encoded by Epstein-Barr
RT virus.";
RL EMBO J. 8:2897-2903(1989).
CC -!- FUNCTION: BARF1 HAS TRANSFORMING ACTIVITY.
CC
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CC
CC EMBL; V01555; CA24809.1; -.
DR PIR; A03792; Q0B548.
DR PIR; S33058; S33058.
DR InterPro; IPR003600; Ig_Like.
DR SMART; SM00410; IG_Like; 1.
KW Early protein; Oncogene.
SQ SEQUENCE 221 AA; 24471 MW; CA5A24D1EA28758E CRC64;

Query Match 11.2%; Score 129; DB 1; Length 221;
Best Local Similarity 27.0%; Pred. No. 0.00054;
Matches 43; Conservative 25; Mismatches 47; Indels 44; Gaps 8;

QY 18 EVATLSCGHNVSVVEELAQRIYVOK-----BKKMVLTMMSGDMNIWPE 60
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 19 QAVTAFLGFRVLTLS-----YWRYSGLGPEIEVSWFKLGPGEQVLGRMHHDV-IFIE 71
QY 61 YKNRTFDI---TNLSIVLALRPSDEGYECVVLKYKDAFKREHLAEV---TLSV-- 112
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 72 WFERGFFDHRNANTFLLVVTANISHDGNLYCRMKLGTEVTKQHLVSVVKPLTSLVHS 131
QY 113 -KADFPPTSISDPEIPTSNIIRICTSGGFPPEHLSWL 150
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 132 ERSQEP-----DFSVLT-----VTCTVNAFPHVQWL 159

RESULT 12
BUTY_HUMAN
ID BUTY_HUMAN STANDARD; PRT; 526 AA.
AC Q13410;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Butyrophilin precursor (BT).
GN BTN1AL OR BTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=96201696; PubMed=8611614;
RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT "Cloning and sequence analysis of human Butyrophilin reveals a
RT potential receptor function.";
RL Biochim. Biophys. Acta 1306:1-4(1996).
CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.

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CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC
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CC
CC EMBL; U39576; AAC50489.1; -.
DR Genew; HGNC:1135; BTN1AL.
DR MIN; G01610; -.
DR InterPro; IPR001870; Gamma_carboxylase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR003878; SPRY_domain.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00622; SPRY; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00449; SPRY; 1.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 26
FT CHAIN 27 526
FT DOMAIN 27 242
FT TRANSMEM 243 269
FT DOMAIN 270 526
FT CARBOHYD 55 55
FT CARBOHYD 215 215
SQ SEQUENCE 526 AA; 59004 MW; E9EACDF8DAF94D5 CRC64;

Query Match 11.1%; Score 127; DB 1; Length 526;
Best Local Similarity 27.5%; Pred. No. 0.0024;
Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps 10;

QY 16 VKEVATLSC--GHNVSVEELAQRIYVQKEKKMWLTMSG---DMNIWPEYKNRTIF--- 67
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 42 VGDAELPCRLSPNASEHL-ELRFRKVKVSPAVLVHRDGRQEAQEMPEYRGRATLVQD 100
QY 68 -DITNLSIVLALRPSDEGYECVVLKYKDAFKREHLAEVTLVSKADFPPTSISDDEI 126
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 101 GIAGRVAIRNGVRVSDDEYTCF---FREDGSVEEL--VHLKVAALGSDPHIS-MQV 154
QY 127 PTSNIIRICTSGGFPPEHLSW-LENGELNAINITVSDPETE-LYAVSSKLDNFMTT 184
DB : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 155 QENGEICLECTSGVWYPEPQVQWRTSKGBKFP--STSESRRNPDEGLFTVAASVIIRDTS 212
QY 185 NHPWCLIK 193
DB : | | |
DB 213 TKNVSCYIQ 221

RESULT 13
CL166_CHICK
ID CL166_CHICK STANDARD; PRT; 588 AA.
AC P42292;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE CL166 antigen precursor (SCL glycoprotein) (BEN glycoprotein) (DM-
DE GRASP protein) (JC7 protein).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
RC TISSUE=Embryo;
RX MEDLINE=92030150; PubMed=1931049;
RA Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
RA McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;

```


Search completed: January 6, 2003, 14:24:26
Job time : 15 secs

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OM protein - protein search, using sw model

Run on: January 6, 2003, 14:22:50 ; Search time 29 Seconds
(without alignments)
1534.696 Million cell updates/sec

Title: US-09-454-651B-23
Perfect score: 1149
Sequence: 1 GLSHFCGVIHVTKRKEVA.....LRVNTFNWNTTKQEHFDPN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.priodont.*
- 12: sp.virus.*
- 13: sp.vertebrate.*
- 14: sp.unclassified.*
- 15: sp.rvirus.*
- 16: sp.bacteriaph.*
- 17: sp.archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1118	97.3	288	6	O77684
2	1100	95.7	288	6	Q28499
3	1085	94.4	288	6	Q9BDN6
4	1085	94.4	289	6	Q28347
5	772	67.2	296	6	Q8WMZ2
6	764	66.5	230	6	Q9N213
7	762.5	66.4	288	6	Q9TT70
8	762.5	66.4	297	6	Q9BE99
9	761	66.2	229	6	Q9TT71
10	743	64.7	292	6	Q9GMZ8
11	743	64.7	292	6	O02758
12	719	62.6	304	6	Q9TOX1
13	717.5	62.4	236	6	O46405
14	705	61.4	235	6	Q9N0T0
15	705	61.4	235	6	Q9TQ58
16	603.5	52.5	321	11	O35187

17	602	52.4	290	11	Q62680	Q62680 rattus norv
18	601.5	52.3	321	11	Q62624	Q62624 rattus norv
19	596	51.9	321	11	O55202	O55202 rattus norv
20	560	48.7	306	11	Q9R129	Q9R129 mus musculus
21	350	30.5	174	6	Q9GMZ9	Q9GMZ9 felis silve
22	349.5	30.4	173	6	Q9SL17	Q9SL17 felis silve
23	255.5	22.2	212	11	Q61332	Q61332 mus musculus
24	200.5	17.4	329	6	Q9XSX6	Q9XSX6 felis silve
25	200.5	17.4	332	6	Q9GMZ7	Q9GMZ7 felis silve
26	200.5	17.4	332	6	Q9SL16	Q9SL16 felis silve
27	188.5	16.4	280	6	Q9TTF1	Q9TTF1 canis famli
28	188.5	16.4	296	13	O42404	O42404 gallus gall
29	182	15.8	329	6	Q9TTF2	Q9TTF2 canis famli
30	178	15.5	323	6	Q9BDM2	Q9BDM2 cercopithec
31	177	15.4	323	6	Q9BDM9	Q9BDM9 macaca neme
32	177	15.4	323	6	Q9EDM4	Q9EDM4 macaca mula
33	176	15.3	275	6	Q9BDN9	Q9BDN9 papio anubi
34	176	15.3	323	6	Q9BDB8	Q9BDB8 cercocebus
35	171	14.9	284	6	Q9GL33	Q9GL33 bos taurus
36	162	14.1	313	11	O35531	O35531 rattus norv
37	161.5	14.1	325	6	O02838	O02838 sus scrofa
38	159	13.8	316	11	Q8VE98	Q8VE98 mus musculu
39	156.5	13.6	290	4	Q9NZQ7	Q9NZQ7 homo sapien
40	153	13.3	290	11	Q9EP73	Q9EP73 mus musculu
41	153	13.3	356	11	Q64381	Q64381 mus musculu
42	152	13.2	314	11	Q61238	Q61238 mus musculu
43	150	13.1	309	11	Q91YV7	Q91YV7 mus musculu
44	142	12.4	316	4	Q9BXR1	Q9BXR1 homo sapien
45	139.5	12.1	521	6	O46651	O46651 oryctolagus

ALIGNMENTS

RESULT 1

O77684	ID	O77684	PRELIMINARY;	PRT;	288 AA.
AC	O77684;				
DT	01-NOV-1998	(Tremblrel. 08, Created)			
DT	01-NOV-1998	(Tremblrel. 08, Last sequence update)			
DT	01-JUN-2002	(Tremblrel. 21, Last annotation update)			
DE	B7 protein.				
DE	B7.				
OS	Macaca nemestrina (Pig-tailed macaque).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;				
OC	Cercopitheidae; Macaca.				
OX	NCBI_TaxID=9545;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Kraus G., Hnatyszyn J.H.;				
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF079519; AAC31555.1; -				
DR	HSSP; P33681; IDR9.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR003600; Ig-like.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF000047; ig; 1.				
DR	SMART; SM00409; IG; 1.				
DR	SMART; SM00410; IG-like; 1.				
SQ	SEQUENCE 288 AA; 33131 MW; 76BBC42839E9AB79 CRC64;				

Query Match 97.3%; Score 1118; DB 6; Length 288;

Best Local Similarity 97.7%; Pred. No. 1.2e-91;

Matches 210; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LSHPFCGVIHVTKRKEVATLSCGHNVSEELAQTRIVYQKREKKVLTMSGDMNINPEY 61
|||||

Db 28 LSHPFCGVIHVTKRKEVATLSCGHNVSEELAQTRIVYQKREKKVLTMSGDMNINPEY 87
|||||

QY 62 KNRTIFDITNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLTSVKADFPPTPSI 121
|||||

Db 88 KNRTIFDITNLSIVILALRPSDEGTCECVLVKYEKDAFKREHLAEVTLTSVKADFPPTPSI 147
|||||

QY 122 SDFEIPSTNIRRIICSTSGGPPHLSWLENGEELNAINNTVSDPETELYAVSSKLDNF 181
 Db :|||||
 Db 148 TDFEIPSPNIRRIICSTSGGPPHLSWLENGEELNAINNTVSDPETELYAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGHRLVNQTFNNTTKQEHFPDN 216
 Db :|||||
 Db 208 MTNHSFMCILIKYGHRLVNQTFNNTTKQEHFPDN 242

RESULT 2

Q28499
 ID Q28499 PRELIMINARY; PRT; 288 AA.
 AC Q28499;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE B7 protein (CD80 protein precursor).
 GN B7 OR N939.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates.";
 RL J. Immunol. 155:3946-3954(1995).
 RN [2]

Query Match 95.7%; Score 1100; DB 6; Length 288;
 Best Local Similarity 96.3%; Pred. No. 4.8e-90;
 Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 2 LSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKWKVLTMMSGDMNIWPEY 61
 Db :|||||
 Db 28 LSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKWKVLTMMSGDMNIWPEY 87
 QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 121
 Db :|||||
 Db 88 KNRTIFDITNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 147
 QY 122 SDFEIPSTNIRRIICSTSGGPPHLSWLENGEELNAINNTVSDPETELYAVSSKLDNF 181
 Db :|||||
 Db 148 TDFEIPSPNIRRIICSTSGGPPHLSWLENGEELNAINNTVSDPETELYAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGHRLVNQTFNNTTKQEHFPDN 216
 Db :|||||
 Db 208 MTNHSFMCILIKYGHRLVNQTFNNTTKQEHFPDN 242

Query Match 95.7%; Score 1100; DB 6; Length 288;
 Best Local Similarity 96.3%; Pred. No. 4.8e-90;
 Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKWKVLTMMSGDMNIWPEY 61
 Db :|||||
 Db 28 LSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKWKVLTMMSGDMNIWPEY 87
 QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 121
 Db :|||||
 Db 88 KNRTIFDITNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 147
 QY 122 SDFEIPSTNIRRIICSTSGGPPHLSWLENGEELNAINNTVSDPETELYAVSSKLDNF 181
 Db :|||||
 Db 148 TDFEIPSPNIRRIICSTSGGPPHLSWLENGEELNAINNTVSDPETELYAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGHRLVNQTFNNTTKQEHFPDN 216
 Db :|||||
 Db 208 MTNHSFMCILIKYGHRLVNQTFNNTTKQEHFPDN 242

RESULT 3

Q9BDN6
 ID Q9BDN6 PRELIMINARY; PRT; 288 AA.
 AC Q9BDN6;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE CD80 protein.
 GN MNB71.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Cercopithecus.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344839; AAK37535.1; -.
 DR HSSP; P33681; IDR9.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00410; IG_like; 1.
 DR SMART; SM00410; IG_like; 1.
 SQ SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 288;
 Best Local Similarity 95.3%; Pred. No. 1e-88;
 Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKWKVLTMMSGDMNIWPEY 61
 Db :|||||
 Db 28 LSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKWKVLTMMSGDMNIWPEY 87
 QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 121
 Db :|||||
 Db 88 KNRTIFDITNLSIVILALRPSDEGTYECVLYKEDAFKREHLAEVTLVSKADFTPSI 147
 QY 122 SDFEIPSTNIRRIICSTSGGPPHLSWLENGEELNAINNTVSDPETELYAVSSKLDNF 181
 Db :|||||
 Db 148 TDFEIPSPNIRRIICSTSGGPPHLSWLENGEELNAINNTVSDPETELYAVSSKLDNF 207
 QY 182 MTNHSFMCILIKYGHRLVNQTFNNTTKQEHFPDN 216
 Db :|||||
 Db 208 MTNHSFMCILIKYGHRLVNQTFNNTTKQEHFPDN 242

RESULT 4

Q28347
 ID Q28347 PRELIMINARY; PRT; 289 AA.
 AC Q28347;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE B7 protein (fragment).
 GN B7.
 OS Cercopithecus torquatus (red-crowned mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Cercopithecus.
 OX NCBI_TaxID=9530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BLOOD;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and


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RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
DR EMBL; U19833; AAA86700.1; -.
DR HSP; P33681; IDR9.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00410; Ig_like; 2.
FT NON_TER 289
SQ SEQUENCE 289 AA; 33030 MW; 5ED6A3F6A3C59297 CRC64;

Query Match
Best Local Similarity 94.4%; Score 1085; DB 6; Length 289;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVIHVTKEVATLSGCHNVSVLELAQTRIIYQKEKKMVLTMGDMNIWPE 61
Db 28 LSHFCSGVIHVTKEVATLSGCHNVSVLELAQTRIIYQKEKKMVLTMGDMNIWPE 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVVLKYKEDAFKREHLAEVTLVKADFPPTPSI 121
Db 88 KNRTIFDITNLSIVILALRPSDEGTYECVVLKYKEDAFKREHLAEVTLVKADFPPTPSI 147
QY 122 SDFEIPTSNIRRIICSTSGGPPPEHLNENALNTVSDPETELVAVSSKLDNF 181
Db 148 TDFEIPPSNIRRIICSTSGGPPPEHLNENALNTVSDPETELVAVSSKLDNF 207
QY 182 MTNHSFVCLIKYGHRLVQTFNNTTKQEHFPDN 216
Db 208 MTNHSFVCLIKYGHRLVQTFNNTTKQEHFPDN 242

RESULT 5
Q8WMZ2
ID Q8WMZ2 PRELIMINARY; PRT; 296 AA.
AC Q8WMZ2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CD80.
GN CD80.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Tadaki D.K., Williams A., Lee K.P., Kirk A.D., Harlan D.M.;
RT direct human T-cell activation."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF45811; AAL58443.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_like; 1.
KW Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 230 POTENTIAL.
SQ SEQUENCE 296 AA; 33275 MW; 69E494237E679C98 CRC64;

Query Match
Best Local Similarity 67.2%; Score 772; DB 6; Length 296;
Matches 141; Conservative 28; Mismatches 42; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSGCHNVSVLELAQTRIIYQKEKKMVLTMGDMNIWPE 60
Db 22 GLDFCSCGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81
QY 61 YKNTIFDITNLSIVILALRPSDEGTYECVVLKYKEDAFKREHLAEVTLVKADFPPTPS 120
Db 82 YENRTFTDVTNNLCIVILALRPSDEGTYECVVLKYKEDAFKREHLAEVTLVKADFPPTPS 141
QY 121 ISDFEIPTSNIRRIICSTSGGPPPEHLNENALNTVSDPETELVAVSSKLDNF 180
Db 142 ITALGNPSNIRRIICSTSGGPPPEHLNENALNTVSDPETELVAVSSKLDNF 201

Query Match
Best Local Similarity 66.8%; Score 772; DB 6; Length 296;
Matches 141; Conservative 28; Mismatches 42; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSGCHNVSVLELAQTRIIYQKEKKMVLTMGDMNIWPE 60
Db 22 GLDFCSCGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81
QY 61 YKNTIFDITNLSIVILALRPSDEGTYECVVLKYKEDAFKREHLAEVTLVKADFPPTPS 120
Db 82 YENRTFTDVTNNLCIVILALRPSDEGTYECVVLKYKEDAFKREHLAEVTLVKADFPPTPS 141
QY 121 ISDFEIPTSNIRRIICSTSGGPPPEHLNENALNTVSDPETELVAVSSKLDNF 180
Db 142 ITALGNPSNIRRIICSTSGGPPPEHLNENALNTVSDPETELVAVSSKLDNF 201

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QY 181 NMTNHSFVCLIKYGHRLVQTFNNTTKQEHFPDN 211
Db 202 NVTGNHSPVCLIKYGHRLVQTFNNTTKQEHFPDN 232

RESULT 6
Q9N2I3
ID Q9N2I3 PRELIMINARY; PRT; 230 AA.
AC Q9N2I3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CD80 protein precursor.
GN CD80/B7.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada M., Amai S., Hoshi M., Nio M., Ohi R.;
RT "Porcine CD80(B-7) mRNA, partial cds."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026121; BAA50700.2; -.
DR HSP; P33681; IDR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00410; Ig_like; 1.
KW Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 230 POTENTIAL.
SQ SEQUENCE 230 AA; 26028 MW; EB63AD172663C4A4 CRC64;

Query Match
Best Local Similarity 66.5%; Score 764; DB 6; Length 230;
Matches 140; Conservative 26; Mismatches 43; Indels 0; Gaps 0;

QY 1 GLSHFCSGVIHVTKEVATLSGCHNVSVLELAQTRIIYQKEKKMVLTMGDMNIWPE 60
Db 22 GLDFCSCGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81
QY 61 YKNTIFDITNLSIVILALRPSDEGTYECVVLKYKEDAFKREHLAEVTLVKADFPPTPS 120
Db 82 YENRTFTDVTNNLCIVILALRPSDEGTYECVVLKYKEDAFKREHLAEVTLVKADFPPTPS 141
QY 121 ISDFEIPTSNIRRIICSTSGGPPPEHLNENALNTVSDPETELVAVSSKLDNF 180
Db 142 ITALGNPSNIRRIICSTSGGPPPEHLNENALNTVSDPETELVAVSSKLDNF 201

Query Match
Best Local Similarity 67.0%; Score 764; DB 6; Length 230;
Matches 140; Conservative 26; Mismatches 43; Indels 0; Gaps 0;

QY 181 NMTNHSFVCLIKYGHRLVQTFNNTTKQEHFPDN 209
Db 202 NVTGNHSPVCLIKYGHRLVQTFNNTTKQEHFPDN 230

RESULT 7
Q9TT70
ID Q9TT70 PRELIMINARY; PRT; 288 AA.
AC Q9TT70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CD80 protein precursor (Fragment).
GN CD80.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

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RP  SEQUENCE FROM N.A.
RX  MEDLINE=20302785; PubMed=10843688;
RA  Faas S.J., Giannoni M.A., Mickle A., Kiesecker C.L., Reed D.J., Wu D.,
RA  Fodor W.L., Mueller J.P., Mattis L.A., Rother R.P.;
RT  "Primary Structure and Functional Characterization of a Soluble,
RL  J. Immunol. 164:6340-6348(2000).
DR  EMBL; AF203443; AAF22750.1; -.
DR  HSP; P33681; 1DR9.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR003600; Ig_Like.
DR  InterPro; IPR003006; Ig_MHC.
DR  Pfam; PF00047; Ig; 2.
DR  SMART; SM00409; Ig; 1.
DR  SMART; SM00410; Ig_Like; 1.
KW  Signal.
FT  SIGNAL.
FT  CHAIN          1 29
FT  NON_TER       30 >288
FT  CD80 PROTEIN.
SQ  SEQUENCE 288 AA; 32510 MW; 67E31D0FDB45D1C8 CRC64;

Query Match      66.4%; Score 762.5; DB 6; Length 288;
Best Local Similarity 66.5%; Pred. No. 5.5e-60;
Matches 141; Conservative 28; Mismatches 42; Indels 1; Gaps 1;

Qy  1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVLELAQTRIVYQKEKKVLTMMSGDMNIWPE 60
Db  22 GLDFCSCGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVWPK 81

Qy  61 YKRTIFDTNNLSIVILALRPSDEGTVCVVKLYEKDAFKREHLAEVTLVSKADFPPTS 120
Db  82 YENRTFTDVTNNLCIVILALRLSDNGTYTCVVKQKRGSGYKLEHLTSVKLMVKADFPVPS 141

Qy  121 ISDFEIPTSNIRRICTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db  142 ITALGNFSPNIRKIRCTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 201

Qy  181 NMTTNHSMCLIKYGHRLVNQTFNW-NTTKQE 211
Db  202 NVTGNHSMCLIKYGHRLVNQTFNW-NTTKQE 233

Qy  181 NMTTNHSMCLIKYGHRLVNQTFNW-NTTKQE 211
Db  202 NVTGNHSMCLIKYGHRLVNQTFNW-NTTKQE 233

RESULT 8
Q9BE99
ID  Q9BE99          PRELIMINARY;      PRT;      297 AA.
AC  Q9BE99;
DT  01-JUN-2001 (Tremblrel. 17, Created)
DT  01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT  01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE  CD80 protein precursor.
GN  CD80/B7-1.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=LANDRACE; TISSUE=ILEUM MUCOSA;
RA  Wada M., Amae S., Sano N., Ishii T., Hoshi M., Sasaki H.,
RA  Hayashi Y., Ohi R.;
RT  "cloning and sequencing of cDNAs for porcine B7-1 (CD80) and soluble
RT  isoforms.";
RL  Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB049760; BAB40952.1; -.
DR  HSP; P33681; 1DR9.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR003600; Ig_Like.
DR  InterPro; IPR003006; Ig_MHC.
DR  Pfam; PF00047; Ig; 2.
DR  SMART; SM00409; Ig; 1.
DR  SMART; SM00410; Ig_Like; 1.
KW  Signal.
FT  SIGNAL.
FT  CHAIN          1 29
FT  POTENTIAL.
FT  CD80 PROTEIN.
SQ  SEQUENCE 288 AA; 32510 MW; 67E31D0FDB45D1C8 CRC64;

Query Match      66.4%; Score 762.5; DB 6; Length 288;
Best Local Similarity 66.5%; Pred. No. 5.5e-60;
Matches 141; Conservative 28; Mismatches 42; Indels 1; Gaps 1;

Qy  1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVLELAQTRIVYQKEKKVLTMMSGDMNIWPE 60
Db  22 GLDFCSCGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVWPK 81

Qy  61 YKRTIFDTNNLSIVILALRPSDEGTVCVVKLYEKDAFKREHLAEVTLVSKADFPPTS 120
Db  82 YENRTFTDVTNNLCIVILALRLSDNGTYTCVVKQKRGSGYKLEHLTSVKLMVKADFPVPS 141

Qy  121 ISDFEIPTSNIRRICTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db  142 ITALGNFSPNIRKIRCTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 201

Qy  181 NMTTNHSMCLIKYGHRLVNQTFNW-NTTKQE 211
Db  202 NVTGNHSMCLIKYGHRLVNQTFNW-NTTKQE 233

Qy  181 NMTTNHSMCLIKYGHRLVNQTFNW-NTTKQE 211
Db  202 NVTGNHSMCLIKYGHRLVNQTFNW-NTTKQE 233

RESULT 9
Q9TT71
ID  Q9TT71          PRELIMINARY;      PRT;      229 AA.
AC  Q9TT71;
DT  01-MAY-2000 (Tremblrel. 13, Created)
DT  01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT  01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE  CD80 protein precursor.
GN  CD80 OR CD80/B7-1.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=SPLEEN;
RA  Wada M., Amae S., Hoshi M., Nio M., Ishii T., Sano N., Sasaki H.,
RA  Ohi R.;
RT  "Splicing Isoform of Porcine CD80.";
RT  Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF203442; AAF22749.1; -.
DR  EMBL; AB038153; BAA90764.1; -.
DR  HSP; P33681; 1DR9.
DR  InterPro; IPR003599; Ig.
DR  InterPro; IPR003600; Ig_Like.
DR  InterPro; IPR003006; Ig_MHC.
DR  Pfam; PF00047; Ig; 2.
DR  SMART; SM00409; Ig; 1.
DR  SMART; SM00410; Ig_Like; 1.
KW  Signal.
FT  SIGNAL.
FT  CHAIN          1 29
FT  CD80 PROTEIN.
SQ  SEQUENCE 229 AA; 25900 MW; C3AD172663C4A4ED CRC64;

Query Match      66.2%; Score 761; DB 6; Length 229;
Best Local Similarity 67.8%; Pred. No. 5.6e-60;
Matches 139; Conservative 26; Mismatches 40; Indels 0; Gaps 0;

Qy  1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVLELAQTRIVYQKEKKVLTMMSGDMNIWPE 60
Db  22 GLDFCSCGIVQVTKVKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVWPK 81

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FT SIGNAL 1 33 POTENTIAL.
FT CHAIN 34 304 B7-1 PROTEIN.
SQ SEQUENCE 304 AA; 34454 MW; 09E082F6BB06C94F CRC64;

Query Match 62.6%; Score 719; DB 6; Length 304;
Best Local Similarity 60.5%; Pred. No. 4.4e-56;
Matches 130; Conservative 36; Mismatches 49; Indels 0; Gaps 0;

QY 2 LSHFCSGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPEY 61
DB 28 LFYFCSGIIQVNTKTVKEAVLSCDYNISTELMKVRIYQKDEVVAVLATVSGQTKVWSKY 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADFPPTPSI 121
DB 88 ENRTFADFTNLSIVIMALRLSDNGKYTCIVQTEKRSYKVHKMTSVMLLVRADEFVPSI 147
QY 122 SDFEIPTSNIRRIICSTSGGFPPEHLVSWLENGEELNAINTVSQDPETELYAVSSKLDNF 191
DB 148 TDLGNPSHDIKRMCTSGGFPKPHLSWNEEELNAINTVSQDPDTELYTISSELDNF 207
QY 182 MTTNHSFCLIKYGHRLVNTQFNWNTTKOEHPDN 216
DB 208 ITSNSHFVCLVKYGLDITVSIQIFNWKSVPEHPNN 242

RESULT 13
O46405 PRELIMINARY; PRT; 296 AA.
ID O46405
AC O46405;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE CD80 antigen precursor (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99115507; PubMed=9914337;
RA Parsons K.R., Howard C.;
RT "Cloning of cattle CD80. ";
RL Immunogenetics 49:231-234(1999).
DR EMBL; Y09950; CAA71081.1; -.
DR HSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_Like; 1.
KW SIGNAL.
FT SIGNAL 1 25 POTENTIAL.
FT NON_TER 296 296
SQ SEQUENCE 296 AA; 33618 MW; 7ADB11FB5F532EF5 CRC64;

Query Match 62.4%; Score 717.5; DB 6; Length 296;
Best Local Similarity 63.2%; Pred. No. 5.8e-56;
Matches 134; Conservative 28; Mismatches 47; Indels 3; Gaps 2;

QY 1 GLSHFCSGVI--HVTKEVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIW 58
DB 27 GLFYFCSGITPKSVTKRKVETVMSLDYNTSTELTSLRIYQKDSKMLAILPGKVQVW 86
QY 59 PEYKNRTIFDITNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADEP 117
DB 87 PEYKNRTIFDITNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADEP 146
QY 118 TPSISDFEIPTSNIRRIICSTSGGFPPEHLVSWLENGEELNAINTVSQDPETELYAVSSK 177
DB 147 VPTINDLGNPSNIRRIICSTSGGFPPEHLVSWLENGEELNAINTVSQDPETELYAVSSK 206

"New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
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QY 178 LDFNMTNHSFCLIKYGHRLVNTQFNWNTTK 209
DB 207 LDFNMTNHSFCLIKYGHRLVNTQFNWNTTK 238

RESULT 14
Q9N0T0 PRELIMINARY; PRT; 235 AA.
ID Q9N0T0
AC Q9N0T0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE T-cell co-stimulatory protein B7-1.
GN B7-1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Carnivora; Flissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Khatlani T., Ma Z., Onishi T.;
RT "Cloning and Sequencing of canine cDNA encoding T-cell co stimulatory molecule B7-1. ";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257653; AAF69006.1; -.
DR HSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00410; IG_Like; 1.
SQ SEQUENCE 235 AA; 26933 MW; C0EA51DA9FB224E3 CRC64;

Query Match 61.4%; Score 705; DB 6; Length 235;
Best Local Similarity 61.5%; Pred. No. 5.7e-55;
Matches 128; Conservative 33; Mismatches 47; Indels 0; Gaps 0;

QY 2 LSHFCSGVIHVTKEVATLSCGHNVSVEELAQTRIVYQKEKKMVLTMMSGDMNIWPEY 61
DB 28 LFYFCSGIIQVNTKTVKEAVLSCDYNISTELMKVRIYQKDEVVAVLATVSGQTKVWSKY 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTYECVVLKYKDAFKREHLAEVTLVSKADFPPTPSI 121
DB 88 ENRTFADFTNLSIVIMALRLSDNGKYTCIVQTEKRSYKVHKMTSVMLLVRADEFVPSI 147
QY 122 SDFEIPTSNIRRIICSTSGGFPPEHLVSWLENGEELNAINTVSQDPETELYAVSSKLDNF 181
DB 148 TDLGNPSHDIKRMCTSGGFPKPHLSWNEEELNAINTVSQDPDTELYTISSELDNF 207
QY 182 MTTNHSFCLIKYGHRLVNTQFNWNTTK 209
DB 208 ITSNSHFVCLVKYGLDITVSIQIFNWKCK 235

RESULT 15
Q9TQ8 PRELIMINARY; PRT; 235 AA.
ID Q9TQ8
AC Q9TQ8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Secreted B7-1 protein precursor.
GN CD80.
OS Canis familiaris (Dog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Carnivora; Flissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
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